

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 22, 2001, 00:18:34 Search time 1471.74 seconds
(without alignments)
6659.142 Million cell updates/sec

Title: US-09-463-480-3

Perfect score: 625

Sequence: 1 gcaatccatcaacagagagg.aaaaa.....aaaaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0 Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl.*

1: qb_bal.*
2: qb_bal.*
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84: qb_vl27.*
85: qb_vl28.*
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87: qb_vl30.*
88: qb_vl31.*
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90: qb_vl33.*
91: qb_vl34.*
92: qb_vl35.*
93: qb_vl36.*
94: qb_vl37.*
95: qb_vl38.*
96: qb_vl39.*
97: qb_vl40.*
98: qb_vl41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	625	12	AF110779
2	66.8	10.7	17839	4	AE001384
3	65.2	10.4	750	93	AL137550 Homo sapi
4	65.2	10.4	321003	84	AL035476 Plasmodiu
5	63.8	10.2	805	53	AL416788 17 end of
6	63.8	10.2	2710	6	X92840 D.melanogas
7	62	9.9	924	53	AL436159 17 end of
8	61.4	9.8	2976	5	U09478 Dictyosteli



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OM nucleic - nucleic search, using sw model

Run on: July 22, 2001, 00:23:09, Search time 52.75 seconds.
(without alignments)
1248.654 Million cell updates/sec

Title: US-09-463-480-3

Perfect score: 625

Sequence: 1 accatccatcaacacagaaqg.....aaaaaaaaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC

Gapop 10 0, Gapext 1 0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_NA.*

- 1: /com2_6/pdata/1/ina/5A.COMB.seq.*
- 2: /com2_6/pdata/1/ina/5B.COMB.seq.*
- 3: /com2_6/pdata/1/ina/6A.COMB.seq.*
- 4: /com2_6/pdata/1/ina/6B.COMB.seq.*
- 5: /com2_6/pdata/1/ina/patents.comb.seq.*
- 6: /com2_6/pdata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.6	9.4	857	1	US-08-308-883-1
2	58.6	9.4	857	1	US-08-730-163-1
3	58.6	9.4	857	4	US-08-256-799-1
4	58.6	9.4	857	4	US-08-462-437-1
5	58.2	9.3	3138	1	US-07-867-106-4
6	56.8	9.1	991	3	US-08-924-747-25
7	56.8	9.1	991	4	US-09-247-2738-25
8	56.8	9.1	991	4	US-09-296-715-25
9	56.6	9.1	1474	4	US-08-821-994-64
10	56.2	9.0	703	4	US-09-313-300-6
11	56.2	9.0	1582	3	US-08-545-1968-10
12	56.2	9.0	1582	3	US-08-545-1968-12
13	56	9.0	1172	1	US-07-945-288-9
14	56	9.0	1172	1	US-08-462-831-9
15	56	9.0	1172	1	US-08-461-809-9
16	56	9.0	1172	1	US-08-461-441-9
17	56	9.0	1172	5	PCT US93 08518-9
18	55.6	8.9	5852	1	US-07-867-106-2
19	55.4	8.9	1578	4	US-09-416-050A-1
20	55.4	8.9	1578	4	US-09-664-800-1
21	55.4	8.9	1578	4	US-09-665-309-1
22	55.2	8.8	3527	2	US-08-909-9552-7
23	54.8	8.8	1534	1	US-08-300-903A-6
24	54.6	8.7	1075	4	US-08-400-0068-6
25	54.2	8.7	2852	3	US-09-027-137-2
26	53.8	8.6	1364	1	US-08-265-087-3
27	53.8	8.6	1364	1	US-08-621-493-3

28	53.8	8.6	1364	2	US-08-965-688-3
29	53.8	8.6	1364	4	US-09-260-173-3
30	53.6	8.6	10660	2	US-08-267-803B-8
31	53.6	8.6	10660	4	US-09-041-886-16
32	53.4	8.5	1046	1	US-08-361-467B-4
33	53.4	8.5	1046	1	US-08-361-467B-4
34	53.2	8.5	1641	1	US-08-300-903A-8
35	53.2	8.5	1776	3	US-08-655-352-10
36	53.2	8.5	5173	1	US-08-242-677-1
37	53	8.5	8920	2	US-08-446-855A-1
38	53	8.5	8920	4	US-09-150-741-1
39	52.8	8.4	1700	2	US-08-897-340-4
40	52.8	8.4	1700	4	US-09-252-229-4
41	52.8	8.4	4238	5	PCT US94 10880-5
42	52.6	8.4	2447	2	US-09-014-969-14
43	52.4	8.4	2550	6	5258287-23
44	52.4	8.4	2887	5	PCT US96 10521-14
45	52.2	8.4	1098	4	US-09-248-335-35

ALIGNMENTS

RESULT 1
US-08-308-883-1
Sequence 1, Application US/08408884
Patent No. 5576400
GENERAL INFORMATION:
APPLICANT: Muketji, P.
APPLICANT: Prieto, P. A.
APPLICANT: Seo, A. E.-Y.
INVENTOR: Baxter, J. H.
APPLICANT: Cummings, R.D.
TITLE OF INVENTION: Method for inhibition of human rotavirus infection.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Louie R. Drayer
ADDRESSEE: KES Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: United States
ZIP: 43215
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: ClarisWorks 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08408883
FILING DATE: 16-Sep-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: No. 5576400 applicable
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 624-3774
TELEFAX: (614) 624-3074
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
DESCRIPTION: Human milk kappa casein
HYPOTHETICAL: No
ANALYSE:
FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM: homo sapiens
STRAIN:
INDIVIDUAL ISOLATE:

Sequence 3, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 16, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 14, Appli
Patent No. 5258287
Sequence 14, Appli
Sequence 35, Appli

Db 839 A 839

```
RESULT 3
US-08-456-799-1
: Sequence 1, Application US/08/256799
: Patent No. 6232094
: GENERAL INFORMATION:
: APPLICANT: HANSSON, Lennart
: APPLICANT: STROEMQVIST, Mats
: APPLICANT: BERGSTROEM, Sven
: APPLICANT: HERNELL, Olie
: APPLICANT: TOERNELL, Jan
: TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
: TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N W, Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/256799
: FILING DATE: 06-DEC-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DK 88/92
: FILING DATE: 23-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: COOPER, Iver P.
: REGISTRATION NUMBER: 28 005
: REFERENCE/DOCKET NUMBER: HANSSON-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 857 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEetical: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 45..593
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 45..543
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 45..104
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 13..44
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 594..848
US-08-256-799-1
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Query Match 9.4%, Score 58.6; DB 4; Length 857.
Best Local Similarity 67.8%; Pred. No. 0.00029;

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Matches 82; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 505 tcttttlaactgagctatttaattttttcaatttttcaacaataaagattatttttaagaa 564
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 719 tcttctctctttaaatttttaatttttaatttttaatttttaatttttaatttttaatttt 778
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 565 tgttaagtattagaaatttttttttttttttttttttttttttttttttttttttttttt 624
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 779 AGCAACTGATTGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 838
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 625 a 625
Db 839 A 839

RESULT 4
US-08-462-437-1
: Sequence 1, Application US/08/462437
: Patent No. 6232094
: GENERAL INFORMATION:
: APPLICANT: HANSSON, Lennart
: APPLICANT: STROEMQVIST, Mats
: APPLICANT: BERGSTROEM, Sven
: APPLICANT: HERNELL, Olie
: APPLICANT: TOERNELL, Jan
: TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
: TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/462437
: FILING DATE: 05-JUN-1995
: INFORMATION FOR SEQ ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 857 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEtical: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 45..593
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 45..593
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 45..104
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Lb 789 CATAAAGTAGATGATTTCTTGGGAACAATATATCTCTGTCGACAAAGGATGT 848
Cy 498 catatagctctttactagactatttattttcaattttccaaataaataattttt 557
Lb 849 TCTGTTTAAATTAATGACGTGATTTGCTTGCTATGCTATTTAAATTTAACTA 908
Cy 558 aatggaatgttaatgattgaataatgaataatgaataatgaataatgaataat 617
Lb 909 AAAAACTCTTCATCTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 968
Cy 618 aaaaaaa 625
Lb 969 AAAAAAA 976

RESULT 7

US-09-247 373B 25
Sequence 25, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 991
TYPE: DNA
ORGANISM: SOYBEAN
US-09-247-373B-25

Query Match 9.1%, Score 56.8, DB 4, Length 991,
Best Local Similarity 56.4%, Pred No. 0.00069,
Matches 106; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Cy 438 catcatagctctgataataattgctcctaaaggagaaattctatgttgcagagaataat 497
Lb 789 cataataagtagatgatttctgttggaacaattatctctgttctgaagaaagattgt 848
Cy 498 catatagctctttactagactatttattttcaattttccaaataaataattttt 557
Lb 849 tctgttttaatttaattgacttgatgttggttggtggtatttgaattttaacta 908
Cy 558 aatggaatgttaatgattgaataatgaataatgaataatgaataatgaataatga 617
Lb 909 aaaaaatgttcaatttttaaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 968
Cy 618 aaaaaaa 625
Lb 969 aaaaaaa 976

RESULT 8

US-09-296-715-25
Sequence 25, Application US/09296715
Patent No. 6171834
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.O. BOX 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/296,715
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/BOOKET NUMBER: CL-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-892-8112
TELEFAX: 402-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: SOYBEAN
IMMEDIATE SOURCE:
CLONE: SSM.PK0067.G5
US-09-296-715-25

Query Match 9.1%, Score 56.8, DB 4, Length 991,
Best Local Similarity 56.4%, Pred No. 0.00069,
Matches 106; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Cy 438 catcatagctctgataataattgctcctaaaggagaaattctatgttgcagagaataat 497
Lb 789 CATAAAGTAGATGATTTCTTGGGAACAATATATCTCTGTCGACAAAGGATGT 848
Cy 498 catatagctctttactagactatttattttcaattttccaaataaataattttt 557
Lb 849 TCTGTTTAAATTAATGACGTGATTTGCTTGCTATGCTATTTAAATTTAACTA 908
Cy 558 aatggaatgttaatgattgaataatgaataatgaataatgaataatgaataatga 617
Lb 909 AAAAACTCTTCATCTTTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 968
Cy 618 aaaaaaa 625
Lb 969 AAAAAAA 976

RESULT 9

US-08-821-994-64
Sequence 64, Application US/08821994A
Patent No. 6228643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-23
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER FILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 64
; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-954-64

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Query Match	9.1%	Score 56.67	D8_4	length 1474
Best Local Similarity	65.4%	Pred. No. 0.0008		
Matches 83:	Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;

QY	499	atatagtcttttactgaagtaattaatatttttcacaaatagaqattatttta	558
Db	1298	atatacattgctgcggaaaagatatgatttgatttatgataggaaatataata	1357
QY	559	atqqatgttaagtatagaaat'gaadadaaaaaaaadadaaaaaa	618
Db	1358	aadatatatatctctatgaadadaaaaaaaadadaaaaaadadaaaa	1417
QY	619	aaadaaa	625
Db	1418	adaaaaa	1424

Query Match	9.0%	Score 56.2	DB 4	Length 703
Best Local Similarity	65.6%	Pred. No. 0.00087		
Matches 82	Conservative 0	Mismatches 43	Indels 0	Gaps 0
QY	501	atagctcttttttactgagctatttlaattttttcaatttcacccaataagagattatttfaat	560	
Db	144	ATTTACTCTTACTGTACATCTTTTACTTTTGAATTTGCCAATAAGGATTTACTCTCAAT	85	
QY	561	qaaaqtatataatataatataatataatataatataatataatataatataatataatataat	620	
Db	84	CTTGTTTCAACTCTCAA	25	
QY	621	aaaaaa	625	
Db	24	AAAAA	20	

1 GENERAL INFORMATION:
 2 APPLICANT: MELKI, JUDITH
 3 APPLICANT: MÜNICH, ARNOLD
 4 TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
 5 TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
 6 NUMBER OF SEQUENCES: 65
 7 CORRESPONDENCE ADDRESS:
 8 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
 9 STREET: PO BOX 747
 10 CITY: FALLS CHURCH
 11 STATE: VA
 12 COUNTRY: USA
 13 ZIP: 22040-0747
 14 COMPUTER READABLE FORM:
 15 MEDIUM TYPE: Floppy disk
 16 COMPUTER: IBM PC compatible
 17 OPERATING SYSTEM: PC-DOS/MS-DOS
 18 SOFTWARE: PictUtil Release #1.0, Version #1.30
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: 05/238/545,196B
 21 FILING DATE: 19-OCT-1995
 22 CLASSIFICATION: 435
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: FARACI, C. J.
 25 REGISTRATION NUMBER: 32,350
 26 REFERENCE/DOCKET NUMBER: 2121-110P
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: (703) 205-8000
 29 TELEFAX: (703) 205-8050
 30 INFORMATION FOR SEQ ID NO: 10:
 31 SEQUENCE CHARACTERISTICS:
 32 LENGTH: 1582 base pairs
 33 TYPE: nucleic acid
 34 STRANDEDNESS: double
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: cDNA
 37 OS-08-545-196B-10

Query Match	9.0%;	Score 56.2;	DB 3;	Length 1582;
Pos-local similarity	65.4%;	Prod No 0	00007;	
Matches 82;	Conservative	0;	Mismatches 43;	Indels 0;
Gaps	0;			
QY	501	atagctctttttactgaqctatttaatttttcaattttccaccaataaagattatttaatt	560	
Db	1424	ATTGTACTCTTTTTTCTCACTCTATATGTTAAAGACTATATAAANAATTTTAATT	1483	
QY	561	gaagatgatttaagtattgaqaatttgaagaaagaaagaaagaaagaaagaaagaaagaa	620	
Db	1484	TTTTTTTAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANA	1543	
QY	621	aaaaa	625	
Db	1544	AAAAA	1548	

RESULT 11
US-08-545-196B-10
; Sequence 10, Application US/08545196B
; Patent No. 6080577

```

1  RESULT 14
2  US-08-462-831-9
3  : Sequence 9, Application US/08462831
4  : Patent No. 5552142
5  : GENERAL INFORMATION:
6  : APPLICANT:
7  : TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
8  : DERMATOPHAGOIDES
9  : NUMBER OF SEQUENCES: 13
10 : CORRESPONDENCE ADDRESS:
11 : ADDRESSEE: LAHIVE & COCKFIELD
12 : STREET: 60 STATE STREET, SUITE 510
13 : CITY: BOSTON
14 : STATE: MA
15 : COUNTRY: USA
16 : ZIP: 02109
17 : COMPUTER READABLE FORM:
18 : MEDIUM TYPE: Floppy disk
19 : COMPUTER: IBM PC Compatible
20 : OPERATING SYSTEM: PC-DOS/MS-DOS
21 : SOFTWARE: ASCII TEXT
22 : CURRENT APPLICATION DATA:
23 : APPLICATION NUMBER: US,08,462,831
24 : FILING DATE:
25 : CLASSIFICATION: 424
26 : PRIOR APPLICATION DATA:
27 : APPLICATION NUMBER: US 07/945,288
28 : FILING DATE: 10 SEPTEMBER 1992
29 : APPLICATION NUMBER: US 580,655
30 : FILING DATE: 11 SEPTEMBER 1990
31 : APPLICATION NUMBER: US 458,642
32 : FILING DATE: 13 FEBRUARY 1990
33 : ATTORNEY/AGENT INFORMATION:
34 : NAME: MANDRAGOURAS, AMY E.
35 : REGISTRATION NUMBER: 36,207

```

1 REFERENCE/LOCKET NUMBER: 1P0 01000 (IM1-024)

2 TELECOMMUNICATION INFORMATION:

3 TELEPHONE: (617) 227-7400

4 TELEFAX: (617) 227-5541

5 INFORMATION FOR SEQ ID NO: 9:

6 SEQUENCE CHARACTERISTICS:

7 LENGTH: 1172 base pairs

8 TYPE: nucleic acid

9 STRANDEDNESS: single

10 TOPOLOGY: linear

11 MOLECULE TYPE: cDNA

12 FEATURE:

13 NAME/KEY: CDS

14 LOCATION: 1..748

15 US-08-462-841-9

Query Match 9.0%; Score 56; DB 1; Length 1172;

Best Local Similarity 61.8%; Pred. No. 0.001;

Matches 89; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 482 atttgcagaaataatcatatagttcttttttactgaagctatttcaatttttcaattttca 541

DB 998 GTGTGTCATTCTCTAAACAAAAGACAAATTCCTTATATGATGTCACAAATTAATTA 1057

QY 542 ccaataagatatttttaaggaatgttaatatattagatataaaaataaaaataaaa 601

DB 1058 TCAAAATTTTAAAGAAATGAAATTAATTCATTCACAAAATTAATAAAAAA 1117

QY 602 aaaaataaaaataaaaataaaaataaaa 625

DB 1118 AAAAAAAAAAAAAAAAAAAAAA 1141

RESULT 15

US-08-461-809-9

Sequence 9, Application US/08461809

Patent No. 5770202

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM

DERMATOPHAGOIDES

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,809

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 458,642

FILING DATE: 18 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGORAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/DECKET NUMBER: 1P0 01000 (IM1-024)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5541

1 INFORMATION FOR SEQ ID NO: 9:

2 SEQUENCE CHARACTERISTICS:

3 LENGTH: 1172 base pairs

4 TYPE: nucleic acid

5 STRANDEDNESS: single

6 TOPOLOGY: linear

7 MOLECULE TYPE: cDNA

8 FEATURE:

9 NAME/KEY: CDS

10 LOCATION: 1..748

11 US-08-461-809-9

Query Match

Best Local Similarity 61.8%; Pred. No. 0.001;

Matches 89; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 482 atttgcagaaataatcatatagttcttttttactgaagctatttcaatttttca 541

DB 998 GTGTGTCATTCTCTAAACAAAAGACAAATTCCTTATATGATGTCACAAATTAATTA 1057

QY 542 ccaataagatatttttaaggaatgttaatatattagatataaaaataaaaataaaa 601

DB 1058 TCAAAATTTTAAAGAAATGAAATTAATTCATTCACAAAATTAATAAAAAA 1117

QY 602 aaaaataaaaataaaaataaaaataaaa 625

DB 1118 AAAAAAAAAAAAAAAAAAAAAA 1141

Search completed: July 22, 2001, 01:41:39

Job time: 4710 sec


```

PI * Umek RM;
XX
DR WP1: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6: Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 17.7%; Score 110.6; DR 22; Length 938;
Best Local Similarity 0.8%; Pred. No. 8,1e-11;
Matches 5; Conservative 394; Mismatches 218; Indels 0; Gaps 0;

QY 9 atcaacaaagatttgaaggaaatccattttatgaagaagatcgaaagaatttactc 59
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 685 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 ttaagatcaacatgaaggaagcagctttttcttctgtctgtctctctctatgatt 128
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 625 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 tcaaaatcgcacatgaagatgaagatgaagatgaagatgaagatgaagatgaag 189
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 565 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 aagcgaagatgaagatgaagatgaagatgaagatgaagatgaagatgaagatga 248
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 505 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 tttgtatttgcacaaatcctatgaagatgaagatgaagatgaagatgaagatga 308
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 445 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 409 aatgaatcctcattatcagaacacatttgaagcgaagcgaagcgaagcgaagcga 368
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 485 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 369 tgaagacatttctcagctcctatgaagatgaagatgaagatgaagatgaagatga 428
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 425 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 429 atcttcacacacacacacacacacacacacacacacacacacacacacacacac 488
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 265 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 489 gaaatcaatcattatgaagatgaagatgaagatgaagatgaagatgaagatgaag 548
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 295 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 549 gatttatttgaagatgaagatgaagatgaagatgaagatgaagatgaagatgaag 608
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 145 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 609 aaaaataaaaataaaaataaaaataaaaataaaaataaaaataaaaataaaaata 625
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 85 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
AAF58252
ID AAF58252 standard; DNA; 946 bp
XX

```

```

AC AAF58252;
XX
XX 24-APR-2001 (first entry)
XX
XX Oligonucleotide D1835.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
XX Synthetic.
XX
XX WC20107665 A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-0520476.
XX
XX 26-JUL-1999; 990S-0145695.
XX
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
XX
XX WP1: 2001 159728/16.
XX
XX Nucleic acids containing electron transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX
XX Example 6: Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
XX acids each containing an electron-transfer group (ETM) having
XX different redox potentials. The invention is used for electronic
XX detection of nucleic acids, especially of substitutions (mismatches)
XX and single nucleotide polymorphisms, e.g. for genotyping,
XX monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 17.5%; Score 109.4; DR 22; Length 936;
Best Local Similarity 0.8%; Pred. No. 1.3e-10;
Matches 5; Conservative 393; Mismatches 219; Indels 0; Gaps 0;

QY 9 atcaacaaagatttgaaggaatccattttatgaagaagatcgaaagaatttactc 68
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 ttaagatcaacatgaagcagcagctttttcttctgtctgtctctctctatgatt 128
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 171 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 tcaaaagcgcacatttgaagatgaagatgaagatgaagatgaagatgaagatgaag 188
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 231 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 aacataactgaattgaacatcgaagcgaatgaacaaagatttcaatgaatgaatga 248
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 tttgtatttgcacaaatcctatgaagatgaagatgaagatgaagatgaagatgaag 308
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 351 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 aatgaatcctcattatcagaacacatttgaagcgaagcgaagcgaagcgaagcga 368
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 411 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 369 tgaagacatttctcagctcctatgaagatgaagatgaagatgaagatgaagatga 428
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 471 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

QY 429 atcttccgcatcagctctatataaattgctccctaaagagaaatctatattgaca 489
Db 531 www. .... 590
QY 489 gaaataatacctatatttttttactgagccttttaatttttcaatttcaagctatgaa 548
Db 591 www. .... 650
QY 549 gattatttaactgaatgttaattatataaattgaaattgaaataaataaataaataa 608
Db 651 www. .... 710
QY 609 aaaaaaataaataaataa 625
Db 711 www. .... 727

RESULT 9
AAF58254
ID AAF58254 standard; DNA; 936 BP.
XX AC AAF58254;
XX XX
CT 24 APR-2001 (first entry)
XX DE Oligonucleotide D1875.
XX KW Electron-transfer group: ETM; mismatch; genotyping;
XX KW gene expression; ss.
XX GS Synthetic.
XX XX
FN W0200107665-A2.
XX PO 01-FEB-2001.
XX XX
PF 26-JUL-2000; 2000WS-US20476.
XX XX
FR 26-JUL-1999; 990S-0145695.
XX PP 17-MAR-2000; 2000US-0190259.
XX XX
FA (CLIN-) CLINICAL MICRO SENSORS INC.
XX PI Onek RM;
XX XX
DR WPI: 2001-159728/16
XX XX
PI Nucleic acids containing electron transfer group, useful as labels in
PI hybridization assays, e.g. for genotyping; allowing repeat analyses on
PI a single surface.
XX PS
XX PS Example 6; Page 127; 159pp; English.
XX XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

```

```

Query Match 17.5%; Score 109.4; DB 22; Length 936;
Best Local Similarity 0.8%; Pred. No. 1,3e-10;
Matches 5; Conservative 93; Mismatches 219; indels 0; Gaps 0;

```

```

QY 9 atcaacagagaggtttaaagtaaaatctatttcattagaaatctaaagaaatctactc 69
Db 111 www. .... 170
QY 63 ttaagatatacaaatagagagggtaagggtttttctttcttcttcttcttcttcttctt 128

```

```

Db 171 www. .... 230
QY 129 tacaacagcgcagcttgaatataaataacagtgcaacctatagattttatagttacaca 188
Db 221 www. .... 290
QY 189 aacataaactgattgaacatcgccgtaaacagaagttcgaqtcuatftaataacaa 248
Db 291 www. .... 350
QY 249 ttgtatttgacacatctaatgtcaaaqtttcaatgtgaaggtttcatatcacacgaacc 308
Db 351 www. .... 410
QY 409 aatagatctctctctctctctctctctctctctctctctctctctctctctctctct 368
Db 411 www. .... 470
QY 469 tgaagcgcctatttctcatgctactcttgaagcattcaaatatgctgaatctctctct 428
Db 471 www. .... 530
QY 429 atcttccgcatcagctctatataaattgctccctaaagagaaatctatattgaca 488
Db 531 www. .... 590
QY 489 gaaataatacctatatttttttactgagccttttaatttttcaatttcaagctatgaa 548
Db 591 www. .... 650
QY 549 gattatttaactgaatgttaattatataaattgaaattgaaataaataaataaataa 608
Db 651 www. .... 710
QY 609 aaaaaaataaataaataa 625
Db 711 www. .... 727

```

```

RESULT 10
AAF58257
ID AAF58257 standard; DNA; 936 BP.
XX AC AAF58257;
XX XX
CT 24 APR-2001 (first entry)
XX DE Oligonucleotide D1954.
XX KW Electron-transfer group: ETM; mismatch; genotyping;
XX KW gene expression; ss.
XX GS Synthetic.
XX XX
FN W0200107665-A2.
XX PP 01-FEB-2001.
XX PF 26-JUL-2000; 2000WS-US20476.
XX XX
PF 26-JUL-1999; 990S-0145695.
XX PP 17-MAR-2000; 2000US-0190259.
XX XX
FA (CLIN-) CLINICAL MICRO SENSORS INC.
XX PI Onek RM;
XX XX
DR WPI: 2001-159728/16.
XX XX
PI Nucleic acids containing electron-transfer group, useful as labels in
PI hybridization assays, e.g. for genotyping; allowing repeat analyses on
PI a single surface.

```


GenCore version 4.5
Copyright (c) 1993 2000 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: July 22, 2001, 09:20:54 ; Search time 1372.91 seconds
(without alignments)
4303 512 Million cell updates/sec

Title: US-09-463-480-3
Perfect score: 625
Sequence: 1 gccatccatcaacagagg.....aaaaaaaaaaaaaaaaaaaaa 625

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 10228115 seqs, 4756426750 residues
Total number of hits satisfying chosen parameters: 23456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	gb_est1.*
2:	gb_est2.*
3:	gb_est3.*
4:	gb_est4.*
5:	gb_est5.*
6:	gb_est6.*
7:	gb_est7.*
8:	gb_est8.*
9:	gb_est9.*
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11:	gb_est11.*
12:	gb_est12.*
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253: qb_est284.*
254: qb_est285.*
255: qb_est286.*
256: qb_est287.*
257: qb_est288.*
258: qb_est289.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

[illegible]



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

DM protein - protein search, using sw model

Run on: July 18, 2001, 17:27:28 / Search time 12.16 seconds
(without alignments)
212,049 Million cell updates/sec

Title: US-09-463-480-4

Perfect score: 685

Sequence:

1 MPAVAVTACVLCMVHKA.....KVAWVVTGPELISGHPDS IRR

Scoring table:

RLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 191259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 191259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 Issued_Patents_AA:*

- 1: /cgn2_e/ptodata/2/taa/aa/comb.pep.*
- 2: /cgn2_e/ptodata/2/taa/aa/comb.pep.*
- 3: /cgn2_e/ptodata/2/taa/aa/comb.pep.*
- 4: /cgn2_e/ptodata/2/taa/aa/comb.pep.*
- 5: /cgn2_e/ptodata/2/taa/aa/comb.pep.*
- 6: /cgn2_e/ptodata/2/taa/aa/comb.pep.*

Pred. No. is the number of results predicted by database to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.5	11.0	530	4	US 08 943 714-12 Sequence 12, Appl
2	69	10.1	830	4	US 08 872-855-11 Sequence 11, Appl
3	69	10.1	833	1	US 08 264-544-6 Sequence 6, Appl
4	69	10.1	833	1	US 08 083-590A-2 Sequence 2, Appl
5	69	10.1	833	1	US 08 465-500-6 Sequence 6, Appl
6	69	10.1	833	2	US 08 346-129-7 Sequence 6, Appl
7	69	10.1	833	2	US 08 346 128 6 Sequence 6, Appl
8	69	10.1	833	3	US 08 532-384-2 Sequence 2, Appl
9	69	10.1	833	3	US 08 893-828-6 Sequence 6, Appl
10	68	9.9	856	1	US 08 228-162-2 Sequence 2, Appl
11	68	9.9	860	1	US 08 692-817-4 Sequence 4, Appl
12	68	9.9	1074	1	US 08 470-058-2 Sequence 2, Appl
13	68	9.9	1074	3	US 09 037-188-2 Sequence 2, Appl
14	68	9.9	1410	2	US 08 470-058-4 Sequence 4, Appl
15	68	9.9	1410	3	US 09 037-188-4 Sequence 4, Appl
16	66.5	9.7	419	3	US 09 100-391-4 Sequence 4, Appl
17	66	9.6	129	1	US 07 945-288-12 Sequence 12, Appl
18	66	9.6	129	1	US 08 462-831-12 Sequence 12, Appl
19	66	9.6	129	1	US 08 461-809-12 Sequence 12, Appl
20	66	9.6	129	5	US 08 461-441-12 Sequence 12, Appl
21	65	9.5	129	5	PCT-US93-08518-12 Sequence 12, Appl
22	66	9.6	145	3	US 08 460-040-6 Sequence 6, Appl
23	66	9.6	146	1	US 07 945-288-4 Sequence 4, Appl
24	66	9.6	146	1	US 08 462 831 4 Sequence 4, Appl
25	66	9.6	146	1	US 08 461-809-4 Sequence 4, Appl
26	66	9.6	146	1	US 08 461-441-4 Sequence 4, Appl
27	55	9.6	146	2	US 08 485 142 4 Sequence 4, Appl

28	66	9.6	146	2	US 08 478-572-4	Sequence 4, Appl
29	66	9.6	146	5	PCT-US93-08518-4	Sequence 4, Appl
30	65	9.5	481	5	PCT-US91-02186-13	Sequence 13, Appl
31	65	9.5	695	2	US 08 701-240-4	Sequence 4, Appl
32	65	9.5	695	4	US 09 138-236-4	Sequence 4, Appl
33	65	9.5	1186	1	US 08 485-568A-4	Sequence 4, Appl
34	65	9.5	1186	1	US 08 357-698-6	Sequence 6, Appl
35	65	9.5	1186	2	US 08 590 554A-4	Sequence 4, Appl
36	65	9.5	1186	2	US 09 184-223-4	Sequence 4, Appl
37	65	9.5	1186	5	PCT-US93-12682-6	Sequence 6, Appl
38	64.5	9.4	539	2	US 09 032-315-1	Sequence 1, Appl
39	64.5	9.4	539	2	US 08 993-318A-1	Sequence 1, Appl
40	64.5	9.4	539	3	US 08 689-421-27	Sequence 27, Appl
41	64.5	9.4	539	4	US 09 399 886 1	Sequence 1, Appl
42	64.5	9.4	539	4	US 09 396-260-1	Sequence 1, Appl
43	64.5	9.4	539	4	US 09 389-528-27	Sequence 27, Appl
44	64.5	9.4	539	4	US 09 181 827A 27	Sequence 27, Appl
45	64	9.3	951	4	US 08 816-346-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1

US-08-943-714-12

: Sequence 12, Application US/08943714

: Patent No. 6187578

: GENERAL INFORMATION:

: APPLICANT: Rlinkovsky, Alexander

: APPLICANT: Herka, Randy

: APPLICANT: Fey, Michael

: APPLICANT: Gellightly, Elizabeth

: APPLICANT: Klotz, Alan

: APPLICANT: Mathisen, Thomas Erik

: APPLICANT: Lammann, Claus

: TITLE OF INVENTION: Carbonyl Phosphates And Nucleic Acids

: TITLE OF INVENTION: Encoding Same

: NUMBER OF SEQUENCES: 12

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: No. 6187578, No. 6187578disk of No. 6187578th America, Inc.

: STREET: 405 Lexington Avenue

: CITY: New York

: STATE: NY

: COUNTRY: USA

: ZIP: 10174

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Diskette

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: DOS

: SOFTWARE: FastSeq for Windows Version 2.0

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US 08 943 714

: FILING DATE: 03-Oct-1997

: CLASSIFICATION: 435

: ALTERNATE/AGENT INFORMATION:

: NAME: Landiris, Elias J

: REGISTRATION NUMBER: 13,728

: REFERENCE/DOCKET NUMBER: 4970,200-US

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 212-867-0123

: TELEFAX: 212-878-9655

: TELEX:

: INFORMATION FOR SEQ ID NO: 12:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 530 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: US-08-943-714-12

Query Match: 11 59, Score 75.5, PP 4, Length 530;
Best Local Similarity: 21.8%; Pred. No. 1.1;

Matches	32;	Conservative	25;	Mismatches	53;	Indels	17;	Gaps	5;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

QY	10	LVLFVWHKAAIAIDKTCNP-----	TDENVQTITGLTGKQDFE	50
DB		: : : : : : : : : : : : :		
DB	315	LVVTVLVNNVAVLDNFCNFIYENMC	ELMELVGLCFPTFVTHFAAPASIT	474
		: : : : : : : : : : : : :		
QY	51	VNLINLYCAOSNVKVSCD-----	GLHTTTPDPHIIIRPLSGTNNCLVNG	100
DB		: : : : : : : : : : : : :		
DB	475	AFNITWSECSESVFVGDDGPEQEDTS	ANIE-HVLPQVIEGTNRVGLGSLDVM	433
		: : : : : : : : : : : : :		
QY	101	SHATLVAF-----KYANEDVPESES	I	120
DB		: : : : : : : : : : : : :		
DB	434	FNGLHLSLQNNITWNNCKIGFETAP	STPL	460
		: : : : : : : : : : : : :		

RESULT 2
US-08-872-855-11
Sequence 11, Application US/08872855
Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearhart, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

Query Match	10.18;	Score 69;	DB 4;	Length 830;
Best Local Similarity	24.69;	Pred. No. 12;		
Matches 30;	Conservative 15;	Mismatches 43;	Indels 44;	Gaps 3;

QY	1	MRAVAVFACVLFGVMWKAALADK-----TCNPTDEMTVTJTTGLTIGG	45
DB	603	MLPVAIVAAVVFQMKRKRAGEKDAAEKNEQNNAVATMHINGSGVGVALLASASLGG	662
QY	46	PGEFFVN I NRI YAGSNVVFQVCTHTFTTHPHITPTSPNTNFIVNRZAFTEZATL	198
DB	663	K-----TGNSGLTFDG-----GNPNIRKTWKRSNNICASAIAAAAAA	703
QY	106	VA 107	
DB	704	AA 705	

RESULT 3
US-08-264-534-6
; Sequence 6, Application US/08264534
; Patent No. 5648464

Query Match 10.1%; Score 69; DB 1; Length 833;
Best Local Similarity 24.6%; Pred. No. 12;
Matches 30; Conservative 15; Mismatches 43; Indels 34; Gaps 3;

QY	1	MRAVAVFACVLCFMWIKALADK-----TCNPTDPMVTQTITGLTIGG	45
DB			
605	MFLVAATAA	VVFCTMKPKPKAFGTAFAPKQENAVATMHNSGVVALASASTGG	664
QY	46	KQEEVNLIINLYCAQSNVAVSTAGIHHTPEIDPHIIRPLSDGTNGCIIVNCJAIISHATL	105
DB			
665	K-----	TGSNSLTEDG-----GNPNIRKTWTUKSVNNICASAAAAAAA	705
QY	106	VA	107
DB			
706	AA	707	

RESULT 4
US-08-083-590A-2
; Sequence, Affiliation US:08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; TITLE OF INVENTION: Therapeutic A
; TITLE OF INVENTION: And Composit
; TITLE OF INVENTION: Nucleic Acids

: NUMBER OF SEQUENCES: 21
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/463,480A
 : FILING DATE: 25-JUN-1993
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mistrock, S. Leslie
 : REGISTRATION NUMBER: 18,872
 : REFERENCE/DOCKET NUMBER: 7326-015
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212 8698864/9741
 : TELEX: 66141 PENNIE
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 833 amino acids
 : TYPE: amino acid
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-083-590A-2

Query Match 10.1%, Score 69, DB 1, Length 833;
 Best Local Similarity 24.6%, Pred. No. 12;
 Matches 30; Conservative 15; Mismatches 43; Indels 34; Gaps 3;
 QY 1 MRVAVFFACVLCMVHKAALADK-----TCNPTDFMVTOTITGLTIGG 45
 Db 605 MPLVAVIAACVFCMKPKPKPAQKTAFAAPKQNEUNAVATMHHSNGVGVVALASASL23 664
 QY 46 KQFEFVNLIINLYCAOSNVKVSCTGLITTEPIDPHIRLSDCTRINCLVNRGAPISHATL 105
 Db 665 K-----TGSNSGLTFDG-----GNPNLIINLWKSNNNICASAAAAA 705
 QY 106 VA 107
 Db 706 AA 707

RESULT 5
 US-08-463-500-6
 : Sequence 6, Application US/08/463,500
 : Patent No. 5789195
 : GENERAL INFORMATION:
 : APPLICANT: Artavanis-Tsakonas, Spyridon
 : APPLICANT: Muskavitch, Marc A. T.
 : APPLICANT: Fehon, Richard G.
 : APPLICANT: Rebay, Ilaria
 : APPLICANT: Blaumel, Cristine M.
 : APPLICANT: Shepard, Scott B.
 : TITLE OF INVENTION: HUMAN NUTCH AND DELTA, BINDING DOMAINS
 : TITLE OF INVENTION: IN TOPOTHYLMIC PROTEINS, AND METHODS BASED THEREON
 : NUMBER OF SEQUENCES: 34
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: PENNIE & EDMONDS
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: NY
 : COUNTRY: USA
 : ZIP: 10036-2711
 : COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/463,500
 : FILING DATE: 05-JUN-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mistrock, S. Leslie
 : REGISTRATION NUMBER: 18,872
 : REFERENCE/DOCKET NUMBER: 7326-034
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 790-9090
 : TELEFAX: (212) 869-8864/9741
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 833 amino acids
 : TYPE: amino acid
 : TOPOLOGY: unknown
 : MOLECULE TYPE: protein
 : US-08-463-500-6

Query Match 10.1%, Score 69; DB 1; Length 833;
 Best Local Similarity 24.6%, Pred. No. 12;
 Matches 30; Conservative 15; Mismatches 43; Indels 34; Gaps 3;
 QY 1 MRVAVFFACVLCMVHKAALADK-----TCNPTDFMVTOTITGLTIGG 45
 Db 605 MPLVAVIAACVFCMKPKPKPAQKTAFAAPKQNEUNAVATMHHSNGVGVVALASASL23 664
 QY 46 KQFEFVNLIINLYCAOSNVKVSCTGLITTEPIDPHIRLSDCTRINCLVNRGAPISHATL 105
 Db 665 K-----TGSNSGLTFDG-----GNPNLIINLWKSNNNICASAAAAA 705
 QY 106 VA 107
 Db 706 AA 707

RESULT 6
 US-08-463-126-6
 : Sequence 6, Application US/08/463,126
 : Patent No. 5849869
 : GENERAL INFORMATION:
 : APPLICANT: Artavanis-Tsakonas, Spyridon et al.
 : TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
 : TITLE OF INVENTION: In Topothylmic Proteins, And Methods Based Thereon
 : NUMBER OF SEQUENCES: 30
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/463,126
 : FILING DATE:
 : CLASSIFICATION: 530
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/791,923
 : FILING DATE: 14-NOV-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mistrock, S. Leslie
 : REGISTRATION NUMBER: 18,872
 : REFERENCE/DOCKET NUMBER: 7326-007


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2y 46 KQFEFVNI INNIYVAQSNVKSVDGLHTTTPDHFIERLSCGIRNFCVHNCAPISHAAL 105
Db 665 K-----TGSNSGLTTPG . GSNILKNTWQFQVNRICVAAAMAAAAA 705
2y 106 VA 107
Db 706 AA 707

RESULT 9
US-08-893-828-6
: Sequence 6, Application US/08893828
: Patent No. 5050922
: GENERAL INFORMATION:
: APPLICANT: Artavanis-Tsakonas, Spyridon
: APPLICANT: Muskavitch, Marc A.T.
: APPLICANT: Felton, Richard G.
: APPLICANT: Rebay, Ilaria
: APPLICANT: Riamuceller, Cristine M.
: APPLICANT: Shepatz, Scott R
: TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
: TITLE OF INVENTION: IN TOPOTHYMIC PROTEINS, AND METHODS BASED THEREON
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PENNIE & EDMONDS
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10046-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/893,828
: FILING DATE: 11-JUL-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Misrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7326-050
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790 9090
: TELEFAX: (212) 869-8864/9741
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 833 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-08-893-828-6

Query Match 10.1%; Score 69; DB 3; Length 833;
Best Local Similarity 24.5%; Pred. No. 12;
Matches 30; Conservative 15; Mismatches 43; Indels 34; Gaps 4;

Qy 1 MRVAVFVFAVLFQCMVHKAAALADK-----TCNPTDFMVITQITIGTG 45
Db 605 MPLVAVIACVVCVMKKKRAQKDAEAKKQNEQNAVATMHNGSGVGVALASASLOG 664
Qy 46 KQFEFVNI INNIYVAQSNVKSVDGLHTTTPDHFIERLSCGIRNFCVHNCAPISHAAL 105
Db 665 K-----TGSNSGLTTPG . GSNILKNTWQFQVNRICVAAAMAAAAA 705
Qy 106 VA 107
Db 706 AA 707

RESULT 10
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US-09-228-162-2
: Sequence 2, Application US/08228162
: Patent No. 5521971
: GENERAL INFORMATION:
: APPLICANT: Attie, Alan D
: APPLICANT: Sturley, Stephen L
: APPLICANT: Grotch, Daniel G
: TITLE OF INVENTION: Soluble LDL Receptor and Gene
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nicholas J. Scay, Quarles & Brady
: STREET: P.O. Box 2113
: CITY: Madison
: STATE: WI
: COUNTRY: USA
: ZIP: 53701-2113
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/228,162
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/925,403
: FILING DATE: 03-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Scay, Nicholas J
: REGISTRATION NUMBER: 27,386
: REFERENCE/DOCKET NUMBER: 5520642826
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (608) 251-5000
: TELEFAX: (608) 251-9166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 356 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-228-162-2

Query Match 9.9%; Score 68; DB 1; Length 356;
Best Local Similarity 24.7%; Pred. No. 5;
Matches 38; Conservative 13; Mismatches 57; Indels 46; Gaps 8;

Qy 8 FAVLVFVFWVHKAAALAD-----HK-----TCNPTDFMVITQITIGTGKQEF 49
Db 202 PHCLSPVTFISSWQCGGPGCKPSDEENCAVATCPDEF---CCSDGNCIHGSRQCDRE 258
Qy 50 EVNLTIRILYCAQSNVKSVDGLHTTTPDHFIERLSCGIRNFCVHNCAPISHAAL 111
Db 259 YQCKMSIEVGVNVILCEGPN-KKK-----HSQPIILIKV-NMAFQCFWDSDEPIKEGG 314
Qy 89 TNPTLVNCAPIASHALVAFKYAMVPSPSITIS 122
Db 315 TNEGIDNNGSGVHCNLDKIGYECICPDGQQLVA 348

RESULT 11
US-08-092-817-4
: Sequence 4, Application US/08092817
: Patent No. 5436926
: GENERAL INFORMATION:
: APPLICANT: RUBINSTEIN, Menachem
: APPLICANT: NOVICK, Daniela
: APPLICANT: TAL, Nathan
: TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
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Query Match          9 68;      Score 68;  DB 2;  Length 1074;
Best Local Similarity 24.7%;  Pred. NO. 22;
Matches 38;  Conservative 57;  Mismatches 46;  Gaps 8;

QY      8  FAVILFCMVHKAALAD-----DK-----TCNPTDFMTQTITGLTIGSKQFF--- 49
DB      202 FHCLSECHHSWFGLGGCPCKSKDFENCAVATCFQDFE---QVSDNCNCHSGWQCHFF 258
QY      50 -----EVLINLNYGAQSNVKSVDGLHTTEPDPHII-----KPLSD-----G 88
DB      259 YDCKDMSDEVCVNVVTICFQGN-PEFQ---HSGECITIDFVNNAPDVPFWISWQFKEGG 314

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09 INTELUNCATLSHVALFVWUACIADLFFSIAJ 122
II III III : :
Lb 315 INEELINNGSHVNDUKIGYECLEPGGOLVA 348

RESULT 13
US-09-037-188-2 Application US-09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2R04
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER US-09-037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., Janis K.

QY . 50 -----EVNLENNLYTAOSNVKVSIGLITTELEHUII-----RPLSD- -----G 88
DB 250 YCKMCS EGVVNTTCEGR-EEK---ESCEIILKVV-PMARECEWLEFIEEM 214
QY 89 TNNLVNNGAPISHALUAFKYAMVPOSEIIS 122
DB 315 TNECLNNNGCSHVCNLEKUYEELCPDEQLVA 448

Search completed: July 18, 2001, 17:28:17
Job time: 49 sec

GenCode version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein protein search, using sw model

Run on: July 18, 2001, 17:27:28 : Search time 21.18 seconds
(without alignments)
361 260 million cell updates/sec

Title: US-09-463-480-4

Perfect score: 685

Sequence: 1 MPAAVAVFAACVLCFQVWVKAA :KYAWDVDPGSEIIEEPIFNC 129

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 6062988 residues

Total number of hits satisfying chosen parameters: 412575

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	685	100.0	128	AA04129	Lily L1 protein sequence
2	116.5	17.0	1048	AA04129	Arabidopsis thaliana
3	116.5	17.0	1129	AA04129	Arabidopsis thaliana
4	116.5	17.0	1193	AA04129	Arabidopsis thaliana
5	114.5	16.7	135	AA01089	Arabidopsis thaliana
6	114	16.6	124	AA04192	Arabidopsis thaliana
7	113.5	16.6	127	AA01090	Arabidopsis thaliana
8	95.5	13.9	70	AA027387	Arabidopsis thaliana
9	95.5	13.9	75	AA011091	Arabidopsis thaliana
10	95.5	13.9	75	AA027387	Arabidopsis thaliana
11	78.5	11.5	419	AA093300	WO 99/07855 SeqID

12	76.5	11.2	264	AA023735	Arabidopsis thaliana
13	76.5	11.2	281	AA023734	Arabidopsis thaliana
14	76.5	11.2	297	AA023733	Arabidopsis thaliana
15	76.5	11.2	317	AA049594	Arabidopsis thaliana
16	76.5	11.2	317	AA049625	Arabidopsis thaliana
17	76.5	11.2	354	AA049593	Arabidopsis thaliana
18	76.5	11.2	354	AA049624	Arabidopsis thaliana
19	76.5	11.2	354	AA049592	Arabidopsis thaliana
20	76.5	11.2	392	AA049623	Arabidopsis thaliana
21	76	11.1	425	AA033559	WO 99/07855 SeqID
22	73.5	10.7	316	AA016590	Arabidopsis thaliana
23	73.5	10.7	536	AA016589	Arabidopsis thaliana
24	73	10.7	2383	AA015945	E. coli proliferat
25	71	10.4	145	AA094865	ber p II antigen f
26	69.5	10.1	800	AA007114	Human low density
27	69	10.1	190	AA033923	Arabidopsis thaliana
28	69	10.1	833	AA028960	Delta D11. Homo s
29	68	9.9	750	AA047868	Human int. receptor
30	68	9.9	939	AA049601	Human low density
31	68	9.9	860	AA047157	Sequence of human
32	68	9.9	860	AA047860	Human LDL receptor
33	68	9.9	924	AA078234	Chicken p95/human
34	68	9.9	1074	AA007621	LDLR/TF chimeric p
35	68	9.9	1410	AA007622	LDLR/TF chimeric p
36	67	9.8	408	AA019760	Pyruvate:ferredoxi
37	67	9.8	519	AA018308	Plasmodium falcipa
38	67	9.8	834	AA079031	Drosophila delta p
39	67	9.8	1395	AA013563	Drosophila Pobo l
40	67	9.8	1395	AA008401	Drosophila sp. ROB
41	66.5	9.7	322	AA022599	LDL receptor fragm
42	66.5	9.7	419	AA041074	Amino acid sequenc
43	66.5	9.7	541	AA022876	YFP-NLS-CP3-multip
44	66.5	9.7	541	AA079654	Caspase-3 biosenso
45	66.5	9.7	6797	AA041598	Pinatoin biosynth

ALIGNMENTS

RESULT 1

AA04129

ID AA04129 standard; Protein; 128 AA.

XX AA04129;

XX 11-MUN-1999 (first entry)

XX Lily L1 protein sequence.

XX Lily L1 protein sequence.

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XX Lily L1 protein sequence.

XX Lily L1 protein sequence.

XX Lily L1 protein sequence.

WT: 1999-142936/12.
N-PSDB: AA019927.
New isolated nucleic acid for, e.g. generating male sterile plants -
comprises a nucleotide sequence that allows expression of a

PF transposase gene in generative and sperm cells of a plant.
 PS Claim 4: Fig 1: 64pp; English.
 XX
 CC The present sequence represents the LGC1 protein from lily (lilium
 CC longiflorum). The sequence specifically allows expression of the
 CC gene in generative and sperm cells of a plant. Also described are: (1) a
 CC genetic construct comprising a generative cell and sperm cell specific
 CC promoter operably linked to a transposase, which is capable of inducing
 CC transposition of a transposable element such that upon expression of the
 CC promoter, the transposase gene is expressed facilitating transposition of the
 CC element; (2) inducing male sterility in a plant by operably linking a
 CC cytotoxic nucleic acid to a promoter, which directs male gamete specific
 CC expression to produce a product from the cytotoxic nucleic acid that
 CC inactivates or kills male gametes in the plant; and (3) a male sterile
 CC plant produced by the method. The male gamete promoter and/or gene is
 CC useful for facilitating male gamete specific transposon tagging, where
 CC the product of pollen grains is screened for a range of phenotypes of
 CC interest, and the transposon tagged plants are used to clone certain
 CC genes. The method is useful for producing seedless fruit or fruit with
 CC reduced seed content, particularly where pollination stimulates fruit
 CC development, and where the lack of fertilisation results in seedless
 CC fruit. The nucleic acids enable specific genetic manipulation of the
 CC male germ line by generating male sterile plants, and facilitating male
 CC gamete specific transposon tagging

XX Sequence 128 AA;

Query Match 100.0%; Score 685; DB 20; Length 128;
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QY 121 ISSDINGS 128
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RESULT 2
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XX AC AAC42154;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 52635.

XX KW Protein identification, signal transduction pathway, metabolic pathway,
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PO 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301430.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0121180.

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RESULT 4
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LT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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CS Arabidopsis thaliana.
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Best Local Similarity 30.5%; Pred. No. 1.1;

Db 11621 EA-----VFETLPADVSASFLLGGCSALTIDIN 1648

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E85822
 C:Species: Escherichia coli
 C:Date: 16 Feb 2001 #sequence_revision 15-Feb-2001 #text_change 21-Mar-2001
 C:Accession: E85822
 R:Kierma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lam, A.; Duanananta, K.; Polamouds, N.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480, MIMD:21074935, PMID:11596551
 A:Accession: E85822
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2660 <STG>
 A:Cross-references: CB A8582274, RIB 312516151, Q136 A8582274, SFLIB 29-07-95, W37 241
 A:Experimental source: strain O157:H7, substrain PDI433
 C:Genetics:
 A:Gene: Z3135

Query Match 10.7% Score 73 DB 2 Length 2660
 Best Local Similarity 29.2% Pred. No. 68
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DB 1838 TVTASMGKSEQLVNFYADTLTAQVNLNVEDNFANNVGMTRQATVTGNGNPLAN 1897

QY 96 NGAPISHTATVAFKYAVDVPPEST-----ISSDN 126

DB 1898 EA-----VFETLPADVSASFLLGGCSALTIDIN 1925

RESULT 11

S69692
 C:Species: Saccharomyces cerevisiae
 C:Date: 22 Aug 1998 #sequence_revision 96-Sep-1996 #text_change 24-Oct-1998
 C:Accession: S69692
 R:Dieffrich, F.S.
 submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9526, 9461, and lamda
 A:Reference number: S69665
 A:Accession: S69692
 A:Molecule type: DNA
 A:Residues: 1-166 <DIE>
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 C:Genetics:
 A:Gene: MIPS:YDR396w
 A:Map position: 4R
 C:Superfamily: Saccharomyces hypothetical protein YDR396w

Query Match 10.6% Score 72.5 DB 2 Length 166
 Best Local Similarity 23.5% Pred. No. 2.8
 Matches 31 Conservative 24 Mismatches 50 Indels 25 Gaps 5

QY 11 VLFQVHKAAADKTCNPT-----DPMVTQTITGLTIGKQEF-----EVNLIINLYCA 60

DB 37 LWCNLDLDELANSCCRSSSSSSFFPFIETLSVSTFWPFIENNISSKNGINSISYN 96

QY 61 QSNVKSSTGLHTTEPDIPIHPSLSGNNVLNNGAP-----ISHATLVAFKYAVDVP 116

DB 97 SSSALITCSG---AMVFLASLSAISEALDRIMNSNPMLMSLASLVNIK----- 145

QY 117 SPSIISSDINCS 128

DB 146 SWSISDIIFT 157

RESULT 12

T48096
 C:Species: Arabidopsis thaliana
 C:Date: 20 Apr 2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48096
 R:Kochowitz, R.; Atkinson-Edler, R.; Leebman, D.; Taitler, R.; Moses, H.W.; Rudd, S.;
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24484
 A:Accession: T48096
 A:Status: preliminary
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 A:Residues: 1-1262 <DB>
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 A:Experimental source: cultivar Columbia; BAC clone T20010
 C:Genetics:
 A:Map position: 3
 A:Introns: 41, 3, 67, 2, 74, 2, 88, 2, 99, 3, 101, 2, 103, 3, 105, 3, 106, 3
 A:Note: T20010 170

Query Match 10.5% Score 72 DB 2 Length 1261
 Best Local Similarity 27.2% Pred. No. 36
 Matches 31 Conservative 16 Mismatches 45 Indels 22 Gaps 5

QY 29 FEFPMVTFITGLTIGKQF-----FVNIINNYAGSNVKSSTGLHTTEPDIPIH 80

DB 496 FSPMSPSVANVQTVSDRGTAVNFHNFETMIDDEVTRAQSN---QLSSIVFTEARVPE 552

QY 81 IIRPLSD--GTNNCLVNNCAPI-----SHATLVAFKYAVDVPPESTIISSDINCS 128

DB 553 VVQGSSESTQGNCLTSETDPIQCSHQSS-----EXHETPLNPDIVNNSANKS 601

RESULT 13

A70729
 C:Species: Mycobacterium tuberculosis
 C:Date: 17 Jul 1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1998
 C:Accession: A70729
 R:Coll, S.T.; Brosch, P.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
 Connor, R.; Davies, R.; Devlin, K.; Fell, W.; T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellern, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, P.; Sulston, T.P.; Taylor, K.; Whitehead, S.; Barrell, R.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MIMD:98295987
 A:Accession: A70729
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-583 <COL>
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 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV2565

Query Match 10.4% Score 71 DB 2 Length 583
 Best Local Similarity 29.0% Pred. No. 18
 Matches 27 Conservative 13 Mismatches 31 Indels 22 Gaps 4

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DB 462 NLNPANMADTGEVTCVLPFTFVPSKGFGLPPIVTPPGIIRPLTCTDNAL-----PP 517

QY 100 ISHATLVAFKYA-----WDVPPSESTIISSDIN 126

DB 518 LOETLLRAFDLAANLANRELPRVAALITEPDVS 550

RESULT 14

138344

Search completed: July 18, 2001, 17:29:07
Job time: 99 sec



GenCore version 4.5
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CM protein - protein search, using sw model

Run on: July 18, 2001, 17:27:28; Search time 11.67 seconds
(without alignments)
375,724 Million cell updates/sec

Title: US-09-463-480-4

Perfect score: 685

Sequence: 1 MRVAVPFACVLCVMHKA.....KYAWDVPSPSTISSINFS 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 94435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	74.5	10.9	1115	1 YAA4_SCHPO	Q09798 schizosacch
2	71	10.4	593	1 YP05_MYCTU	Q6733 mycobacteri
3	69	10.1	833	1 DL_DROME	P18041 Drosophila
4	69	10.1	1788	1 YP72_CABLL	Q6722 baccharid
5	68	9.9	187	1 VGG_BPAL3	P11281 bacterioph
6	68	9.9	860	1 LDLR_HUMAN	P01130 homo sapien
7	67	9.8	617	1 FXK1_MOUSE	P42128 mus musculu
8	67	9.8	648	1 TKT_MYCPN	P75611 mycoplasma
9	66.5	9.7	216	1 O5P4_HUMAN	Q09662 homo sapien
10	66	9.6	146	1 DER2_DERPT	P49278 dermatopha
11	66	9.6	276	1 PIPR_PASHA	Q08869 pasteurella
12	66	9.5	531	1 PEPT_ASPNG	P52718 aspergillus
13	66	9.5	662	1 DCHS_HUMAN	P19113 homo sapien
14	65	9.5	255	1 EL3B_SGYHR	P52095 glycerol max
15	65	9.5	381	1 NCK2_HUMAN	Q43639 homo sapien
16	65	9.5	858	1 ENV_HV2RO	P04577 human immun
17	65	9.5	1186	1 CRAA_BACTS	Q45710 bacillus th
18	64.5	9.4	643	1 Y9C3_METJA	Q53113 methanobact
19	64.5	9.4	738	1 YAS9_SCHPO	Q10145 schizosacch
20	64.5	9.4	863	1 LVPF_CHICK	P48165 gallus gall
21	64.5	9.4	1664	1 SLP1_CLOTM	Q06952 clostridium
22	64	9.3	951	1 HEX_ADE05	P04133 human auto
23	64	9.3	1465	1 A7B7_HUMAN	P55670 homo sapien
24	63.5	9.3	407	1 AK2_BACST	P53553 bacillus st
25	63.5	9.3	701	1 YIA5_YEAST	P40557 saccharomy
26	63.5	9.3	970	1 T3RE_RPPI	P08764 bacterioph
27	63	9.2	573	1 H1FA_HAELN	P11729 haemophilu
28	63	9.2	346	1 POS_PAT	P17438 catenulace
29	62.5	9.1	321	1 AENA_ASPNG	P42256 aspergillus
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32	62.5	9.1	854	1 LDLR_ORIGR	P45950 oryza sativ
33	62	9.1	198	1 Y569_PYRHO	Q58904 pythorocys

34	62	9.1	346	1 RDS_MOUSE	P15499 mus musculu
35	62	9.1	431	1 AK_CHLIR	Q04367 chlamydia t
36	62	9.1	400	1 MYC_BOVIN	Q9T43 bos taurus
37	62	9.1	662	1 DCHS_MOUSE	P23738 mus musculu
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39	61.5	9.0	417	1 SUCB_PIG	P53590 sus scrofa
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42	61	8.9	187	1 VGG_BPHK	Q48042 bacterioph
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ALIGNMENTS

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DT 01-OCT-1996 (Rel. 34, Last annotation update)					
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RN [1]					
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RC STRAIN-972;					
RA Redrock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;					
RL Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.					
CC -! SIMILARITY: TO YEAST PAN2 AND TO C.ELEGANS F31E3.4.					

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL: 254328; CAA91128.1; -					
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DR InterPro: IPR001394; -					
DR Pfam: PF00929; Exonuclease; 1.					
DR Pfam: PF00443; DCH-2; 1.					
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KW Hypothetical protein.					
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10- 140 LSHKRAKAVDILQER ELKDSISIEELHFDNDFIVKRVAVITGLSIDKCN 218					
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OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Rotatoria; Chromadorea; Khabditida; Khabditidae.
 CC Khabditidae; Polidromina; Caenorhabditis.
 CX NCBI_TaxID: 6200.
 FN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN: RW1501, N2.
 RA Lohmrich D., Walterston R.
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBEM databases
 CC
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 CC
 DR EMBL: D24169; AAC08806.1
 DR WormPop: B0228.2; G80:743.
 KW Hypothetical protein.
 SQ SEQUENCE 1788 AA: 200633 MW: 86744346AE19B20A2 CRG64;
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 QY 63 NQVKS--LGLHTI---EPIDRHII 82
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 RESULT 5
 V06_BVAL3
 ID V06_BVAL3 STANDARD; PRT; 187 AA.
 AC P41281;
 DT 01-JUL-1994 (rel. 26, Created)
 DT 01-JUL-1994 (rel. 26, Last sequence update)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DE MAJOR SPIKE PROTEIN (G PROTEIN) (GPC).
 GN G.
 OS Bacteriophage alpha-4.
 OS Viruses; ssDNA viruses; Microviridae; Microvirus.
 CX NCBI_TaxID: 10849;
 FN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:92224109; PubMed:153298.
 RA Kodaira K.-I., Nakano K., Okada S., Taketo A.;
 RT "Nucleotide sequence of the genome of the bacteriophage alpha 4;
 RT interrelationship of the genome structure and the gene products with
 RT those of the phages, phi X174, G4 and phi K2;
 RA Brocchini, Biophys. Acta 113:277-288(1992).
 RL [2]
 RP PARTIAL SEQUENCE.
 RX MEDLINE:80049950; PubMed:387790;
 RA Sims J., Capon D., Dressler D.;
 RT "dnaG (phage)-dependent origins of DNA replication. Nucleotide
 RT sequences of the negative strand initiation sites of bacteriophages
 RT SF-1, phi K2 and alpha 4.";
 RL J. Biol. Chem. 254:12615-12628(1979).
 CC -1- FUNCTION: MAJOR SPIKE COMPONENT. INVOLVED IN THE ATTACHMENT TO
 CC THE BACTERIAL HOST.
 CC -2- SUBUNIT: THE VIRION IS COMPOSED OF 60 COPIES EACH OF THE 12.5 S AND
 CC 3.5 S PROTEINS, AND 12 COPIES OF THE 11 PROTEIN. THERE ARE 12 SPIKES
 CC WHICH ARE EACH COMPOSED OF 5 G AND ONE H PROTEINS.
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 CC
 DR EMBL: X63222; G2A12882.1;
 DR PIR: C04253; C04253.
 DR PIR: S22331; S22331.
 DR BSSP: P04643; IAL0.
 KW Coat protein.
 SQ SEQUENCE 187 AA: 19585 MW: 66748964F7758EF CRG64;
 Query Match 9.9%; Score 68; DB 1; Length 187;
 Best Local Similarity 28.0%; Pred. No. 32;
 Matches 28; Conservative 11; Mismatches 49; Indels 22; Gaps 5;
 QY 47 LLLGLLGGKQKQFVNNLNINIAQS 79
 DB 19 SVTGNVIPAAPTUNTHIVNGSIIAERAVNNLY ANNVSTSSSGSFIAMKVVPTSTDP 77
 QY 80 HIRPLSLSGTNNLYNNIAPISDAIIIAFKVAMDVPESES 119
 DB 78 NCV--ISAGVNLSEAGTSYPI--VGIIVPESESSEQPTSLA 114
 RESULT 6
 LDLR_HUMAN
 ID LDLR_HUMAN STANDARD; PRT; 860 AA.
 AC P01130;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
 GN LDLR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID: 9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:85024898; PubMed:6091915;
 RA Yamamoto T., Davis C.G., Brown M.S., Schneider W.L., Casey M.L.,
 RA Goldstein J.L., Russell D.W.;
 RT "The human LDL receptor: a cysteine rich protein with multiple Ala
 RT sequences in its mRNA.";
 RL Cell 39:27-38(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:85218750; PubMed:2988123;
 RA Suckhot T.C., Goldstein J.L., Brown M.S., Russell D.W.;
 RT "The LDL receptor gene: a mosaic of exons shared with different
 RT proteins.";
 RL Science 228:815-822(1985).
 RN [3]
 RP NCTADINESIS OF CYTOPLASMIC DOMAIN.
 RX MEDLINE:87166314; PubMed:3104386;
 RA Davis C.G., van Griel J.F., Russell D.W., Brown M.S., Goldstein J.L.;
 RT "The low density lipoprotein receptor. Identification of amino acids
 RT in cytoplasmic domain required for rapid endocytosis.";
 RL J. Biol. Chem. 262:4075-4082(1987).
 RN [4]
 RP O-GLYCOSYLATION DOMAIN.
 RX MEDLINE:96140336; PubMed:3005267;
 RA Davis C.G., Ellhammer A., Russell D.W., Schneider W.L., Kornfeld S.;
 RT "Detection of clustered O-linked carbohydrates does not impair
 RT function of low density lipoprotein receptor in transfected
 RT fibroblasts.";
 RL J. Biol. Chem. 261:2828-2838(1986).
 RN [5]
 RP STRUCTURE BY NMR OF 20-67.

EX MEDLINE-95327641; PubMed=7603001;
FA Daly N.J., Scallan M.J., Djordjevic J.T., Kroon P.A., Smith P.;
FI "Three-dimensional structure of a cysteine-rich repeat from the low-
FI density lipoprotein receptor."; J. Biol. Chem. 269:16330-16338(1994)
FL [6]
FN STRUCTURE BY NMR OF 65-104
EX MEDLINE-96062511; PubMed=7578052;
FA Daly N.J., Djordjevic J.T., Kroon P.A., Smith P.;
FI "Three-dimensional structure of the second cysteine-rich repeat from
FI the human low-density lipoprotein receptor."; J. Biol. Chem. 269:16330-16338(1994)
FL [7]
FN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 19c 212.
EX MEDLINE-97404319; PubMed=9262405;
FA Fass D., Blacklow S.C., Kim P.S., Berger J.M.;
FI "Molecular basis of familial hypercholesterolemia from structure of
FI LDL receptor module."; Nature 388:661-664(1997)
FL [8]
FN REVIEW ON FH VARIANTS.
EX MEDLINE-93750847; PubMed=1301956;
FA Hobbs H.H., Brown M.S., Goldstein J.L.;
FI "Molecular genetics of the LDL receptor gene in familial
FI hypercholesterolemia."; Hum. Mutat. 1:445-466(1992)
FL [9]
FN REVIEW ON FH VARIANTS.
EX MEDLINE-97763488; PubMed=9616531;
FA Varret M., Fares J.-P., Colod-Beroud G., Dupont L., Berrouin C.,
FA Beroud C.;
FI "Software and database for the analysis of mutations in the human LDL
FI receptor gene."; Nucleic Acids Res. 25:172-180(1997).
FL [10]
FN VARIANTS FH AFRIKANER-1; -2 AND -3.
EX MEDLINE-89340934; PubMed=2569482;
FA Leitersdorf E., van der Westhuyzen D.P., Coetzee G.A., Parks H.H.;
FI "Two common low density lipoprotein receptor gene mutations cause
FI familial hypercholesterolemia in Afrikaners."; J. Clin. Invest. 84:954-961(1989).
FL [11]
FN VARIANTS FH BARI.
EX MEDLINE-86161691; PubMed=3955657;
FA Davis C.G., Lehrman M.A., Russell D.W., Anderson R.G.W., Brown M.S.,
FA Goldstein J.L.;
FI "The J.E. mutation in familial hypercholesterolemia: amino acid
FI substitution in cytoplasmic domain impedes internalization of LDL
FI receptors."; Cell 45:15-24(1986).
FL [12]
FN VARIANTS FH DIPPAN-1 AND -2.
EX MEDLINE-93350005; PubMed=8347889;
FA Rubinstein D.C., Itai I., Leitersdorf E., Coetzee G.A.,
FA van der Westhuyzen D.P.;
FI "Identification of two new LDL-receptor mutations causing homozygous
FI familial hypercholesterolemia in a South African of Indian origin.";
FL Biochim Biophys Acta 1182:75-82(1993).
FN [13]
FN VARIANTS FH FRENCH CANADIAN-2; -3 AND -4.
EX MEDLINE-90203205; PubMed=2318661;
FA Leitersdorf E., Robin E.J., Davignon J., Hobbs H.H.;
FI "Common low-density lipoprotein receptor mutations in the French
FI Canadian population."; J. Clin. Invest. 85:1014-1024(1990)
FL [14]
FN VARIANTS FH OSAKA-3.
EX MEDLINE-93078772; PubMed=1446662;
FA Miyake Y., Tajima S., Funahashi T., Yamamura T., Yamamoto A.;
FI "A point mutation of low-density-lipoprotein receptor causing rapid
FI degradation of the receptor."; Eur. J. Biochem. 210:17(1992)
FL [15]
FN VARIANTS FH SWEDISH LYS-277, THR-423 AND ASN-579.
EX MEDLINE-95362239; PubMed=7635461;
FA [16]
FN VARIANT FH PISCATAWAY.
EX MEDLINE-91428152; PubMed=1867400;
FA Meiner V., Landsberger D., Berkman N., Peshef A., Sedal P.,
FA Seftel H.C., van der Westhuyzen D.P., Joensuu M.S., Coetzee G.A.,
FA Leitersdorf E.;
FI "A common Lithuanian mutation causing familial hypercholesterolemia
FI in Ashkenazi Jews."; Am. J. Hum. Genet. 49:443-449(1991)
FL [16]
FN VARIANT FH SAFED.
EX MEDLINE-93216279; PubMed=8462973;
FA Leitersdorf E., Peshef A., Meiner V., Dann E.J., Beigel Y.,
FA van der Westhuyzen D.P., Coetzee G.A.;
FI "A missense mutation in the low density lipoprotein receptor gene
FI causes familial hypercholesterolemia in Sephardic Jews."; Hum. Genet. 91:141-147(1993).
FL [17]
FN VARIANT FH TRIESTE.
EX MEDLINE-9422419; PubMed=8168830;
FA Felli N., Garuti P., Pedrazzi P., Ghisellini M., Simone M.I.,
FA Tiozzo R., Cattin L., Valenti M., Rrolleri M., Bertolini S.,
FA Stefanutti C., Calandra S.;
FI "A new missense mutation (Cys297>>Phe) of the low density
FI lipoprotein receptor in Italian patients with familial
FI hypercholesterolemia (FHTrieste)."; Hum. Genet. 93:538-540(1994)
FL [18]
FN VARIANT FH ZAMBIA.
EX MEDLINE-89264579; PubMed=2705768;
FA Soutar A.K., Knight R.L., Patel D.D.;
FI "Identification of a point mutation in growth factor repeat C of the
FI low density lipoprotein receptor gene in a patient with homozygous
FI familial hypercholesterolemia that affects ligand binding and
FI intracellular movement of receptors."; Proc. Natl. Acad. Sci. U.S.A. 86:4166-4170(1989).
FL [19]
FN VARIANTS FH ZAMBIA.
EX MEDLINE-9330622; PubMed=1464748;
FA Felioussin F., Coetzee G.A., Marais A.D., Leitersdorf E.,
FA Seftel H.C., van der Westhuyzen D.P.;
FI "Identification and properties of the proline664-leucine mutant LDL
FI receptor in South Africans of Indian origin."; J. Lipid Res. 33:1647-1655(1992).
FL [20]
FN VARIANTS FH PORT HIS-401 AND TURK ASP-844
EX MEDLINE-96029270; PubMed=7573037;
FA Kuivisto U.-M., Vilkari J.S., Kontula K.;
FI "Molecular characterization of minor gene rearrangements in Finnish
FI patients with heterozygous familial hypercholesterolemia:
FI Identification of two common missense mutations (Gly823>>Asp and
FI Leu380>>His) and eight rare mutations of the LDL receptor gene."; Am. J. Hum. Genet. 57:789-797(1995).
FL [21]
FN VARIANTS FH LYS-140; SER-408 AND LEU-685.
EX MEDLINE-9601600; PubMed=7883548;
FA Maruyama T., Miyake Y., Tajima S., Harada-Shiba M., Yamamura T.,
FA Tsushima M., Kishino K.-I., Higuchi Y., Funahashi T., Matsuzawa Y.,
FA Yamamoto A.;
FI "Common mutations in the low-density-lipoprotein-receptor gene
FI causing familial hypercholesterolemia in the Japanese population."; Arterioscler. Thromb. Vasc. Biol. 15:1713-1718(1995).
FL [22]
FN VARIANTS FH FRENCH HIS-564.
EX MEDLINE-96055524; PubMed=7550239;
FA Tricot-Guher F., Saint-Jore H., Valenti K., Poulton T., Bost M.,
FA Hadian A.J.;
FI "Identification of a mutation, N543H, in exon 11 of the low-density
FI lipoprotein receptor gene in a French family with familial
FI hypercholesterolemia."; Hum. Mutat. 6:87-88(1995).
FL [23]
FN VARIANTS FH SWEDISH LYS-277, THR-423 AND ASN-579.
EX MEDLINE-95362239; PubMed=7635461;
FA [24]

RA Ekstrom U., Abrahamson M., Szeiger T., Lombardi P., Nilsson-Ehle P.;
 RT "An efficient screening procedure detecting six novel mutations in
 RT the LDL receptor gene in Swedish children with
 RT hypercholesterolemia";
 RL Hum. Genet., 96:147-150(1995).
 RP VARIANT FH NORVEGIAN ASN-487 DEL.
 RX MEDLINE: 95362260; PubMed: 7635482;
 RA Leron T.P., Solberg K., Reinberg O.K., Jonstad S., Gao F.;
 RT "Two novel point mutations in the EGF precursor homology domain of
 Query Match 9.9%; Score 68; DB 1; Length 860;
 Best Local Similarity 24.7%; Pred. No. 19;
 Matches 38; Conservative 13; Mismatches 57; Indels 46; Gaps 8;
 QY 8 PACVLCFVHKAALAD-----DK-----TCNPTDPMVVTOTFGLTIGKQKEF---49
 DB 202 PACTLSPEFHSSWPTGSGRKKKSDENAVATCRPFF---QCSQENIHQSPQDRE 258
 QY 50 -----EVNLLNNLYCAQSNVKSVDGLHTTPIPHIL-----KPLSD-----G 88
 DB 259 YDCKMSRNVGVVNTLFGKPN-KFKC---HSGFTILPKVKNMARPDPWNSPPIKEG 314
 QY 89 TNNCLVNNCAPISHATLVAFKYAMDVPSPESIIIS 122
 DB 315 TNECLNNGGCGSHVGNLKIYGECLCPGGLVLA 348
 RESULT 7
 FXKL_MOUSE
 ID FXKL_MOUSE STANDARD; PRT: 617 AA.
 AC P42128;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 34, Last annotation update)
 DE FORHEAD BOX PROTEIN K1 (MYOCYTE NUCLEAR FACTOR) (MNF).
 GN FOXK1 OR MNF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94277065; PubMed=8007964;
 RA Bassel-Duby P., Hernandez M.P., Yang Q., Rochelle J.M.,
 RA Seldin M.F., Williams R.S.;
 PT "Myocyte nuclear factor, a novel myeloid-leukia transcription factor
 RT under both developmental and neural regulation in striated
 RT myocytes";
 RL Mol. Cell. Biol., 14:4536-4605(1994).
 CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE UPSTREAM
 CC ENHANCER REGION (CCAC BOX) OF MYOGLOBIN GENE, HAS A ROLE IN
 CC MYOCYTE DIFFERENTIATION AND IN FETAL BLOOD PROGENES OF ADULT
 CC MUSCLES THAT OCCUR IN RESPONSE TO PHYSIOLOGICAL STIMULI.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING PROBABLY EXISTS, GIVING
 CC RISE TO TWO DIFFERENT TRANSCRIPTS.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN TISSUES AND CELLS IN WHICH THE
 CC MYOGLOBIN GENE IS TRANSCRIPTIONALLY ACTIVE (CARDIAC AND SKELETAL
 CC MYOCYTES, BRAIN, KIDNEY, ...).
 CC -!- PTM: PHOSPHORYLATED.
 CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 FHA DOMAIN.
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 DB EMBL: L26507; AAA37529.1;

DR MGD: MGI:1347488; Foxk1.
 DR InterPro: IPR000253; -;
 DR InterPro: IPR001766; -;
 DR Pfam: PF00498; FHA; 1.
 DR Pfam: PF00250; Fork head; 1.
 DR PRINTS: PR00053; FPKHEAD.
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PROSITE: PS50039; FORK_HEAD_3; 1.
 DR PROSITE: PS50000; FHA_DOMAIN; 1.
 KW DNA-binding; Transcription regulation; Activator, Nuclear protein;
 KW Phosphorylation; Alternative splicing; Differentiation.
 FT DOMAIN 27 33 POLY-ALA.
 FT DOMAIN 107 159 FHA.
 FT DNA_BIND 288 379 FORK-HEAD.
 SQ SEQUENCE 617 AA: 65839 MW: A1083H28C709FC4A CRC64;
 Query Match 9.8%; Score 67; DB 1; Length 617;
 Best Local Similarity 24.2%; Pred. No. 16;
 Matches 24; Conservative 11; Mismatches 38; Indels 26; Gaps 4;
 QY 45 KQKEF-----EVNLLNNLYCAQSNVKSVC-----DGLHTTPIPHILRPLSD; 88
 DB 358 KKGSEWPTDPAFAKIVLQAFKPKPQKGVSCFPTPEGPISSRSPASPTHPGLMSPRSSG 417
 QY 89 --TNNCLVNNCAPISH-----ATLVAFKYAMDVPSP 117
 DB 418 LQTECLSRGSPHPHDIDGSKLASVEFYKYSQSPGS 456
 RESULT 8
 TKT_MYCPN
 ID TKT_MYCPN STANDARD; PRT: 648 AA.
 AC P75611;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSCRIPTASE (PC 2.2.1.1) (TK).
 GN TKT OR TKTA OR MNOR2 OR MPO73.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SIKAIR.A.35:343-343; M129;
 RX MEDLINE=97105887; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Flaegens H., Pirkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae";
 RL Nucleic Acids Res., 24:4120-4149(1996).
 CC -!- CATALYTIC ACTIVITY: SEDHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
 CC 3-PHOSPHATE = D-RIBOSE 5-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE.
 CC -!- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -!- SIMILARITY: BELONGS TO THE TRANSCRIPTASE FAMILY.
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 DB EMBL: AB000009; AAB95721.1;
 DR HSSP: P23254; TKR.
 DR InterPro: IPR000360; -;
 DR Pfam: PF00436; Transcriptase; 3.
 DR PROSITE: PS00801; TRANSCRIPTASE_1; FALSE_NEG.
 DR PROSITE: PS00802; TRANSCRIPTASE_2; 1.
 KW Transferase; Thiamine pyrophosphate.


```

ID 541R SOYBN STANDARD: PRI: 255 AA.
AC P52995;
DI 01-OCT-1996 (rel. 44, Last sequence update)
DI 01-OCT-1996 (rel. 44, Last sequence update)
DI 01 NOV 1997 (rel. 45, Last annotation update)
DE GLUCAN ENDO-1,4-BETA-GLUCOSYLASE (EC 3.2.1.46) (CLC4) BETA-GLUCAN
DE ENDOHYDROLASE) ((1-3)-BETA-GLUCANASE) (BETA 1,4-ENDOGLUCANASE)
DE (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; Eufrosids 1;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
OX NCBI_TaxID 3847;
RN [1]
RP SEQUENCE FROM N.A.
RE STRAIN CV. CENTURY 84; TISSUE Leaf;
RX MEDLINE:95218610; PubMed:776605;
RA Kalinski A., Kowley D.L., Low D.S., Foley C., Pata G., Herman E.M.;
RT "Binding-protein expression is subject to temporal, developmental and
RT stress induced regulation in terminally differentiated soybean
RT nodules";
PL Planta 195;611-621(1995).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
CC IN 1,4-BETA-D-GLUCANS.
CC -1- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL: U08415; AAA1955.1;
DR HSSP: P15747; IGHS.
DR InterPro: IPR000490;
DR Pfam: PF00332; Glyco_Hydro_17; 1.
DR PROSITE: PS00587; GLYCOSYL_HYDROL_F17; 1.
KW Hydrolase; Glycosidase; Multicene family.
FT NON_TER 1
FT ACT_SITE 183 184 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 255 AA: 27671 MW: 124248FPF183G11C CRC64;

Query Match 9.5%; Score 65; DR 1; Length 255;
Best Local Similarity 26.48; Pred. No. 9.5;
Matches 24; Conservative 19; Mismatches 26; Indels 22; Gaps 6;

QY 52 NLINLYCAQSNVKS-----DKLHTTEPDPHRIHLSGCTNRLVNNQ 97
| | | | | | | | | | | | | | | | | | | | | |
DB 65 NTONAISKKEIKVSAIDSLILNSYDNDGVESD AEFY IKFTI NPLVSNQ 118
| | | | | | | | | | | | | | | | | | | | | |

QY 98 APISHATLVAKYKARD--VPPSESLISSDIN 126
| | | | | | | | | | | | | | | | | | | | | |
DB 119 APLIANVYVFAYANDQSIPLAYALFTQOGN 149
| | | | | | | | | | | | | | | | | | | | | |

RESULT 15
N*K2 HUMAN
ID N*K2_HUMAN STANDARD: PRI: 381 AA.
AC 043639;
DI 01-OCT-2000 (rel. 40, Created)
DI 01-OCT-2000 (rel. 40, Last sequence update)
DI 01-OCT-2000 (rel. 40, Last annotation update)
DE CYTOSOLASMIC PROTEIN NCK2 (NCK ADAPTER PROTEIN 2) (CD253B) ADAPT-1-B
DE PROTEIN NCK-BETA).
GN NCK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

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RP SEQUENCE FROM N.A.
RX MEDLINE-98411415; PubMed 9747977;
RA Chen M., She H., Davis E.M., Spicer C.M., Kim L., Ren K., Lebeau M.M.,
RA Li W.;
RT "Identification of NCK family genes, chromosomal localization,
RT expression, and signaling specificity.";
RL J. Biol. Chem. 273:25171-25178(1998).
CC -1- FUNCTION: ADAPTER PROTEIN WHICH ASSOCIATES WITH TYROSINE
CC PHOSPHORYLATED GROWTH FACTOR RECEPTORS OR THEIR CELLULAR
CC SUBSTRATES.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.
CC -1- TISSUE SPECIFICITY: DRUGITIOUS.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 SH3 DOMAINS.
CC
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CC
CC EMBL: AF043119; AAC04841.1;
DR MIM: 604940;
DR HSSP: P19174; IHSO.
DR InterPro: IPR000980;
DR InterPro: IPR001452;
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 3.
DR PROSITE: PS00452; SH3_2; 1.
DR PROSITE: PS00001; SH2; 1.
DR PROSITE: PS00002; SH3; 3.
KW SH3 domain; SH2 domain.
FT DOMAIN 2 62 SH3.
FT DOMAIN 121 171 SH3.
FT DOMAIN 196 258 SH3.
FT DOMAIN 286 380 SH2.
SQ SEQUENCE 481 AA: 43013 MW: 990588EA5AFA5714 CRC64;

Query Match 9.5%; Score 65; DR 1; Length 481;
Best Local Similarity 29.9%; Pred. No. 15;
Matches 18; Conservative 11; Mismatches 20; Indels 12; Gaps 3;

QY 21 LADDEKTNPTDFMYTDTTCTTCTCTGKQ-DEFEVNLINLYCAQSNVKS-DLHTTEPDP 79
| | | | | | | | | | | | | | | | | | | | | |
DB 410 LIPSESSPSFSVS-----LKASGKMKRFAVLIVNVV-----LQPRFTHMELVE 458
| | | | | | | | | | | | | | | | | | | | | |

QY 80 H 80
|
DB 359 H 359

Search completed: July 18, 2001, 17:29:24
Job time: 116 sec

```

GenCore version 4.5
Copyright (c) 1993-2000 CompuLink Ltd.

OM protein - protein search, using sw model

Run on: July 18, 1991, 17:27:28 ; Search time 211.6 seconds
(without alignments)
802 600 million cells

Title: US-09-463-480 4

Perfect score:

Sequence: 1 MRVAVVFACVLFCMVHKA...RTAWVFI...LADVH...D

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs. 132305927 residues

Total number of hills satisfying chosen parameters: 425626

Minimum DB seq length: 0

[illegible]

post-processing: Minimum Match 0%

Processing. Minimum Match 0%
Maximum Match 100%

MAXIMUM PAGE 1008
Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phase:*
- 10: sp.plant:*
- 11: sp.podiatid:*
- 12: sp.unclassified:*
- 13: sp.invertebrate:*
- 14: sp.virus:*

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	685	100	0	128	10	Q4QF17	Q4QF17 Homo sapien
2	134	19	0	124	10	Q4Q393	Q4Q393 Arabidopsis
3	129	18.9	0	123	10	Q4Q392	Q4Q392 Arabidopsis
4	124	18	0	263	10	Q4Q3B1	Q4Q3B1 Arabidopsis
5	116.5	17.0	0	1193	10	Q4MA43	Q4MA43 Arabidopsis
6	78.5	11.5	4	419	11	Q70572	Q70572 mus musculus
7	77.5	11.3	835	11	Q4Q293	Q4Q293 mus musculus	
8	77.5	11.3	835	11	Q4QK6	Q4QK6 mus musculus	
9	76.5	11.2	333	10	Q4FH30	Q4FH30 Arabidopsis	
10	76	11.1	423	4	Q60906	Q60906 homo sapien	
11	75.5	11.0	835	11	Q4QZ45	Q4QZ45 mus musculus	
12	75	10.9	922	3	Q42861	Q42861 schizosacch	
13	74	10.8	1086	5	Q47302	Q47302 plasmodium	
14	73	10.7	2349	2	Q44750	Q44750 escherichia	
15	73	10.7	2383	2	F76347	F76347 escherichia	
16	72.5	10.6	166	3	Q13522	Q13522 saccharomyce	
17	72	10.5	1261	10	Q4LYB5	Q4LYB5 Arabidopsis	
18	71	10.4	535	2	Q4X4D1	Q4X4D1 actinomyces	
19	71	10.4	2927	4	Q10456	Q10456 homo sapien	

ALIGNMENTS

```

RESULT 1
ID QZPJ7 PRELIMINARY, FRG 128 AA.
AC QZPJ7;
DT 01-MAY-1999 (TREMBlrel, 10, created)
DT 01-MAY-1999 (TREMBlrel, 10, last sequence update)
DT 01-MAY-1999 (TREMBlrel, 10, last annotation update)
DE Lili.
GN Lili.
OS Lilium longiflorum (Trumpet Lily).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
OX NCBI_TaxID:4690;
RN [1]
RF SEQUENCE FROM N.A.
RA MAGRINE:44762644; PubMed:10051681;
RA Xu H., Swoboda T., Bhalla P.L., Singh M.B.:
RT "Male gametic cell-specific gene expression in flowering plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2554-2558(1999).
DR EMBL: AF110779; AAC19962.1; ...
SQ SEQUENCE 128 AA, 13851 MW, 4P8694LCTDNCB2314 CRC64;

QZPJ7 Match 100.0% Score 625, DB 10, Length 128;
Best Local Similarity 100.0%; Prod. No. 1e-68; 0; Mismatches 0; Gaps 0;
Matched 128, Conservative 0;

QY 1 MPAVAFACVLCFMMHRAALAKTKTNPTEFMYTQTITGTHGKQFFVNI INNLCA 60
|||||
|||

PT 1 MPAVAFACVLCFMMHRAALAKTKTNPTEFMYTQTITGTHGKQFFVNI INNLCA 60
|||||
|||

QY 61 QSNVKSVCGLHHITLFDHHTLRLSGTINNCILYNNGAPISHATLVAKYAVDVPFESF 120
|||||
|||||
|||||

DB 61 QSNVKSVCGLHHITLFDHHTLRLSGTINNCILYNNGAPISHATLVAKYAVDVPFESF 120
|||||
|||||
|||||

QY 121 ISSDINGS 128
|||||

DB 121 ISSDINGS 128
|||||

RESULT 2
QZPJ7
049383

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Q9MA43
ID Q9MA43 PRELIMINARY: PRT: 1193 AA.
AC Q9MA43;
DI 01-OCT-2000 (FEBRELEL. 15, Created)
DI 01-OCT-2000 (FEBRELEL. 15, Last sequence update)
DI 01-MAR-2001 (FEBRELEL. 16, Last annotation update)
DE T20M3.10 PROTEIN.
GN T20M3.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids ii;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S. X., Sakano H., Yu G., Toriumi M., Leng C., Lee J. M., Li J.,
RA Liu A., Gonzalez A., Liu P., Vaynsberg M., Chin C., Wong H., Choi E.,
RA Chou J., Pham P., Koo T., Altrafi H., Brooks S., Buellier E., Chao Q.,
RA Conn L., Conway A. R., Hansen N., Johnson-Hopson C., Khan S., Kim C.,
RA Lam B., Nguyen M., Palm C., Shinn P., Tambunga G., Davis R. W.,
RA Ecker J. R., Federlspiel N. A., Theologis A.;
RA "Arabidopsis thaliana chromosome 3 BAC 129M3 sequence."
RI Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC009999; AAF29390.1;
DR InterPro: IPR000413;
DR InterPro: IPR000445;
DR InterPro: IPR001214;
DR InterPro: IPR001965;
DR Pfam: PF00855; PWWP; 1;
DR Pfam: PF00856; SET; 1;
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN.1;
DR SMART: SM00249; PHD; 1;
SQ SEQUENCE 1193 AA: 135416 MW: 4F2R3D5776A30DF6 CQVGI;

Query Match 17.0%; Score 116.5; DB 10; Length 1193;
Best Local Similarity 27.8%; Pred. No. 0.00026;
Matches 35; Conservative 17; Mismatches 51; Indels 23; Gaps 5;

QY 3 AVAVTFACV----- IFCVHKALADKNTCNPTDFMVTCTTCTTCTTCTGK 45
DB 1057 ASVVQTCVQMSKPLKFLWSSALILGSSCAICPKSKSPPA---VPLTGVVWPEEKK 1114
QY 47 QFEVNLNLNLYCAGSNVYKVSQDGLHTPEIDPHIPLPSDGINNCLVNNKZATISHAIL 105
DB 1114 --PRVEMNKKPCMPIINLRKCGP-POSTLVDPFLRLVSSAGNCVNDGLDIPSPQI 1170
QY 106 VAPKYA 111
DB 1171 LSENY 1176

RESULT 6
ID Q70572 PRELIMINARY: PRT: 419 AA.
AC Q70572;
DI 01-AUG-1998 (FEBRELEL. 07, Created)
DI 01-AUG-1998 (FEBRELEL. 07, Last sequence update)
DI 01-MAR-2001 (FEBRELEL. 16, Last annotation update)
DE SPHINGOMYELIN PHOSPHODIESTERASE 2 (EC 3.1.4.12) (NEUTRAL
DE SPHINGOMYELINASE) (NSMASE).
GN SMPD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; CHARACTERIZATION, AND TISSUE SPECIFICITY.
RC MEDLINE=98188255; PubMed=9520418;
RA Tomiak S., Hoffman E., Nix M., Galante M., Skoloff W.;
RA "Cloned mammalian neutral sphingomyelinase: functions in sphingolipid
RT signaling?";

Proc. Natl. Acad. Sci. U.S.A. 95:3638-3643(1998).
CC 1- FUNCTION: CONVERTS SPHINGOMYELIN TO CERAMIDE.
CC 1- CATALYTIC ACTIVITY: SPHINGOMYELIN + H(2)O = N-ACYLSPHINGOSINE +
CC CHOLINE PHOSPHATE.
CC 1- COFACTOR: MAGNESIUM.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC 1- TISSUE SPECIFICITY: ALTHOUGH WIDELY EXPRESSED IN ALL TISSUES
CC EXAMINED, EXCEPT THE SPLEEN, HIGH ENZYMATIC ACTIVITY OCCURS ONLY
CC IN THE BRAIN.
CC 1- MISCELLANEOUS: THIS PROTEIN HAS AN OPTIMUM PH OF 6.5-7.5.
CC 1- MISCELLANEOUS: HERE ARE TWO TYPES OF SPHINGOMYELINASES: ASM
CC (ACID), AND NSM (NEUTRAL).
CC 1- SIMILARITY: TO OTHER SPHINGOMYELINASES.
DR EMBL: AJ222800; CAA10994.1;
DR M3D: M3T1279340; Smpd2.
KW Hydrolase; Transmembrane; Magnesium.
FT TRANSMEM 426 406
FT TRANSHEM 354 374
FT METAL 49 49
FT SITE 190 180
FT SITE 190 180
FT AGL SITE 272 272
SQ SEQUENCE 419 AA: 47466 MW: 5812F0B30A69C556 CQC64;

Query Match 11.5%; Score 78.5; DB 11; Length 419;
Best Local Similarity 29.8%; Pred. No. 1.3;
Matches 22; Conservative 7; Mismatches 40; Indels 19; Gaps 2;

QY 23 DDKTNPDPMPVQTITGLTGKQFEVNLNINLYCAGSNVYKVSQDGLHTPEIDPHI 82
DB 212 DDCIMVYKNSYSSQDGLHTPEIDPHIPLPSDGINNCLVNNKZATISHAIL 266
QY 93 EFLSDTRFLVNNCAFLSHATLVAPKYAWDVEP 116
DB 267 KPESD-----HEALMALLYKHSPP 286

RESULT 7
ID Q9Z203 PRELIMINARY: PRT: 835 AA.
AC Q9Z203;
DI 01-MAY-1999 (FEBRELEL. 10, Created)
DI 01-MAY-1999 (FEBRELEL. 10, Last sequence update)
DI 01-MAR-2001 (FEBRELEL. 16, Last annotation update)
DE TOLL-LIKE RECEPTOR 4 MUTANT.
GN LPS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ;
RC MEDLINE=9905147;
RA Poltorak A., Smirnova I., He X., Liu M.-Y., Van Huel C.,
RA Hrdewell P., Alejos E., Silva M., Du X., Thompson P., Chan E. K. L.,
RA Ledesma J., Bee B., Clifton S., Vogel S. N., Beutler L.;
RT "Genetic and physical mapping of the lps locus: identification of the
RT toll-4 receptor as a candidate gene in the critical region.";
EL PNAS 95:24349-24355(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=9905147;
RA Poltorak A., He X., Smirnova I., Liu M.-Y., Van Huel C., Du X.,
RA Birdwell D., Alejos E., Silva M., Galanos C., Freudenberg M.,
RA Ricciardi-Castagnoli P., Layton B., Beutler L.;
RT "Defective lps signaling in C3H/HeJ and C57BL/6J mice: mutations
RT in toll-4 gene.";
EL Science 282:2085-2088(1998).
DR EMBL: AF095453; AAC99411.1;
DR InterPro: IPR000157; -;

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DR INTERP: IPR000484;
DR INTERP: IPR000887;
DR INTERP: IPR001611;
DR PLAM: PR000560; LRR: 7;
DR PLAM: PR01463; LRR: 1;
DR PLAM: PR01582; TIR: 1;
DR PRINTS: PR00019; LEUKICHRPT;
DR PROSITE: PS00159; ALDOSE_KMG_1; UNKN_WN_1;
KW RECEPTOR;
FW VARIANF 712 712 H -- P;
SU SEQUENCE 835 AA: 95558 MW: 969545911A4A0C17 CRC64;

Query Match
Best Local Similarity 26.98; Pred. No. 3.7; Length 845;
Matches 39; Conservative 14; Mismatches 43; Indels 49; Gaps 8;

QY 21 LAUGKCNIDTDMVTGTTGLTGKQKFEVNLNLYAGSNVVSQ---DELH--- 72
DB 205 LSLDMSLNDIDTQQAQVGIK-----HELTGRNF--NSSNIMKTCLNLAHLRHRL 257
QY 73 -----TTEPDIHITRISDOT-----NNGVNGAPISHATL 105
DB 258 ILGEFKERNLEIFESIMEGLCTVIIDEFKLYTINFSGIVAFKELAN---VSAMSL 313
QY 106 --VAFYAWDPSPSILIS-SDIN* 127
DB 314 AGVSTKYLEIDVKKFKWQSLSTIRC 338

RESULT 8
Q9QUR6 PRELIMINARY: PRI: 835 AA.
AC Q9QUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TOLL-LIKE RECEPTOR 4;
GN TLR4;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID: 10090;
RN 11;
RP SEQUENCE FROM N.A.;
RC STRAIN-129;
RA Poltorak A., Smirnova I., Chan E.K.L., Bentler B.;
RT "Genetic variation at the TLR4 locus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.;
RC STRAIN-129;
RA Poltorak A., Smirnova I., Chan E.K.L., Bentler B.;
RT "Genetic variation at the TLR4 locus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

QY 18 KAALADDKTNPIDPMVTGTTGLTGKQKFEVNLNLYAGSNVVSQ---SNVKSQDG 70
DB 169 KCAALMGEGPVYGVLDVQKRVAG-----NFIHVRGLNIYVACMIFGSKNNVNS-HM 220
QY 71 LHTTE-+LIDPHILKPLSINATNNGVNGAPISHATLVAFKYAMV-VDPSEFISSH 125
DB 221 THQLSFGRKYPGTHNPLDQINPIL-----HDSISGIFKYITFVPEYKSKNW 269

RESULT 10
Q9QUR6 PRELIMINARY: PRI: 423 AA.
AC Q9QUR6;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE SPHINGOMYELIN PHOSPHOLIPASE 2 (L3 3.1.4.12) (NEUTRAL
DE SPHINGOMYELINASE) (NSMASE);

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SU SEQUENCE 835 AA: 95558 MW: 969545911A4A0C17 CRC64;

Query Match
Best Local Similarity 11.48; Score 77.5; DB 11; Length 845;
Matches 39; Conservative 14; Mismatches 43; Indels 49; Gaps 8;

QY 21 LAUGKCNIDTDMVTGTTGLTGKQKFEVNLNLYAGSNVVSQ---DELH--- 72
DB 205 LSLDMSLNDIDTQQAQVGIK-----HELTGRNF--NSSNIMKTCLNLAHLRHRL 257
QY 73 -----TTEPDIHITRISDOT-----NNGVNGAPISHATL 105
DB 258 ILGEFKERNLEIFESIMEGLCTVIIDEFKLYTINFSGIVAFKELAN---VSAMSL 313
QY 106 --VAFYAWDPSPSILIS-SDIN* 127
DB 314 AGVSTKYLEIDVKKFKWQSLSTIRC 338

RESULT 9
Q9PH30 PRELIMINARY: PRI: 333 AA.
AC Q9PH30;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BIAAF34232.1;
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Eurosid 11;
OC Brassicales; Brassicaceae; Arabidopsids;
OX NCBI_TaxID: 3702;
RN 11;
RP SEQUENCE FROM N.A.;
RC STRAIN-COLUMBIA;
EX MEDLINE 29277480; PubMed 10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 4. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:141-145 (2000);
DR EMBL: AB022215; HAI17274.1;
SU SEQUENCE 333 AA: 37450 MW: 86621350B0B40B9 CRC64;

Query Match
Best Local Similarity 40.58; Score 76.5; DB 10; Length 333;
Matches 36; Conservative 11; Mismatches 44; Indels 27; Gaps 8;

QY 18 KAALADDKTNPIDPMVTGTTGLTGKQKFEVNLNLYAGSNVVSQ---SNVKSQDG 70
DB 169 KCAALMGEGPVYGVLDVQKRVAG-----NFIHVRGLNIYVACMIFGSKNNVNS-HM 220
QY 71 LHTTE-+LIDPHILKPLSINATNNGVNGAPISHATLVAFKYAMV-VDPSEFISSH 125
DB 221 THQLSFGRKYPGTHNPLDQINPIL-----HDSISGIFKYITFVPEYKSKNW 269

RESULT 10
Q9QUR6 PRELIMINARY: PRI: 423 AA.
AC Q9QUR6;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE SPHINGOMYELIN PHOSPHOLIPASE 2 (L3 3.1.4.12) (NEUTRAL
DE SPHINGOMYELINASE) (NSMASE);

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RESULT 13
>97302
ID 097302 PRELIMINARY: PRT: 1086 AA.
AC 097302
DT 01-MAY-1999 (TREMBL: 10, Created)
DT 01-MAY-1999 (TREMBL: 10, Last sequence update)
DE 01-MAR-2001 (TREMBL: 16, Last annotation update)
DE PFC1045C PROTEIN.
GN PFC1045C.
OS Plasmodium falciparum (isolate 467).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID:46429;
RN 111
RF STRAIN:307;
RA Oliver K., Bowman S., Harris D., Lawson D., Quail M., Bartell R.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBP databases.
DR EMBL: AL044559; CAB4943.1;
DR InterPro: IPR000561;
DR PROSITE: PS01186; EGF_2; UNKN_WN_2;
SQ SEQUENCE 1086 AA: 125841 MW: 125841 MW: RFLPPDARGRGRL94 CR664;

Query Match
Best Local Similarity 10.8%; Score 74; DB 5; Length 1086;
Matches 42; Conservative 13; Mismatches 39; Indels 58; Gaps 7;

QY 4 VAVFF-----ACVLLQMVHKAALAEKQNTPEIMVTQTITGLTIDPKLFEVRLIN 56
DQ 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 81 IRTFSHNRKMSDYF--TSKYSNSSEI---NCTVKKLFEQVWIRNGLLEKLEILN 116
QY 57 --LYAC-----SNVVSSEI-----SNVVSSEI-----EHL 74
DB 136 DKLCAHNSHTLIYISQPLLEPHVVYEIEFEKGNQDINQGMYSIRGSVHVHTH 195
QY 75 EPIDPH--TIRPLSGGNNC 92
DB 196 NALQSEITLYIFNLQCKNNC 217

RESULT 14
ID 094750 PRELIMINARY: PRT: 2343 AA
AC 094750
DT 01-MAY-1997 (TREMBL: 03, Created)
DT 01-MAY-1997 (TREMBL: 03, Last sequence update)
DE 01-MAR-2001 (TREMBL: 16, Last annotation update)
DE INVASIN (FRAGMENT).
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID:562;
RN 111
RF STRAIN:K12;
RA Hoshino K., Baba T., Fujita K., Hayashi K., Honjo A., Horuchi T.,
RA Kasai H., Kobori K., Isono K., Isobe S., Itoh K., Kanai K., Kasai H.,
RA Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,
RA Masuda S., Mori H., Mizoguchi K., Mori H., Motomura K., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sanger G., Sasaki Y.,
RA Takeda H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
FI Submitted (JAN-1997) to the EMBL/GenBank/DBP databases.
DR EMBL: AF000289; AAC76042.1;
DR EMBL: D90837; BAA15800.1;
DR InterPro: IPR000601;
DR InterPro: IPR003444;
DR InterPro: IPR004535;
DR Pfam: PF02369; Bfq_1; 14;
DR PRINTS: PR01369; INTIMIN.
DR SMART: SM00089; PKD; 1;
SQ SEQUENCE 2363 AA: 251391 MW: 1299534 MW: 422562 CR664;

Query Match
Best Local Similarity 10.7%; Score 73; DB 2; Length 2363;
Matches 28; Conservative 10; Mismatches 44; Indels 14; Gaps 3;

QY 47 TITGLTIGKQKPEFVNLIINLYAQSNVSKVSCRLHTTEIDPHLRPLSGNNINLVN 95
DB 153 TVIASMTGKSKSEQLVNFETAITLTAQVNLVTFIDFANNVGMTRLOATVTRHRIPLAN 1620
QY 96 NGAPISHATLVAFKYAWIVPSSESI-----ISSDIN 126
DB 1621 EA-----VTFILPAIVSASFTLGQGGSAITDIN 1648

Search completed: July 18, 2001, 17:28:45
Job time: 77 sec

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FT NON_TER 2349 2349
SQ SEQUENCE 2349 AA: 247433 MW: 125841 MW: RFLPPDARGRGRL94 CR664;

Query Match
Best Local Similarity 10.7%; Score 73; DB 2; Length 2349;
Matches 28; Conservative 10; Mismatches 44; Indels 14; Gaps 3;

QY 47 TITGLTIGKQKPEFVNLIINLYAQSNVSKVSCRLHTTEIDPHLRPLSGNNINLVN 95
DB 153 TVIASMTGKSKSEQLVNFETAITLTAQVNLVTFIDFANNVGMTRLOATVTRHRIPLAN 1604
QY 96 NGAPISHATLVAFKYAWIVPSSESI-----ISSDIN 126
DB 1605 EA-----VTFILPAIVSASFTLGQGGSAITDIN 1642

RESULT 15
ID 076447 PRELIMINARY: PRT: 2483 AA.
AC 076447
DT 01-FEB-1997 (TREMBL: 02, Created)
DT 01-FEB-1997 (TREMBL: 02, Last sequence update)
DT 01-MAR-2001 (TREMBL: 16, Last annotation update)
DE 02483.
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID:562;
RN 111
RF STRAIN:K-12;
RA Blattner F.P., Plunkett G., Plunkett G.P., Bonica N.T., Glasner F.D.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBP databases.
RN 121
RP SEQUENCE OF 2118-2483 FROM N.A.
RC STRAIN:K12;
RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horuchi T.,
RA Itoh K., Kobori K., Isono K., Isobe S., Itoh K., Kanai K., Kasai H.,
RA Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,
RA Masuda S., Mori H., Mizoguchi K., Mori H., Motomura K., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sanger G., Sasaki Y.,
RA Takeda H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
FI Submitted (JAN-1997) to the EMBL/GenBank/DBP databases.
DR EMBL: AF000289; AAC76042.1;
DR EMBL: D90837; BAA15800.1;
DR InterPro: IPR000601;
DR InterPro: IPR003444;
DR InterPro: IPR004535;
DR Pfam: PF02369; Bfq_1; 14;
DR PRINTS: PR01369; INTIMIN.
DR SMART: SM00089; PKD; 1;
SQ SEQUENCE 2363 AA: 251391 MW: 1299534 MW: 422562 CR664;

Query Match
Best Local Similarity 10.7%; Score 73; DB 2; Length 2363;
Matches 28; Conservative 10; Mismatches 44; Indels 14; Gaps 3;

QY 47 TITGLTIGKQKPEFVNLIINLYAQSNVSKVSCRLHTTEIDPHLRPLSGNNINLVN 95
DB 153 TVIASMTGKSKSEQLVNFETAITLTAQVNLVTFIDFANNVGMTRLOATVTRHRIPLAN 1620
QY 96 NGAPISHATLVAFKYAWIVPSSESI-----ISSDIN 126
DB 1621 EA-----VTFILPAIVSASFTLGQGGSAITDIN 1648

Search completed: July 18, 2001, 17:28:45
Job time: 77 sec

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